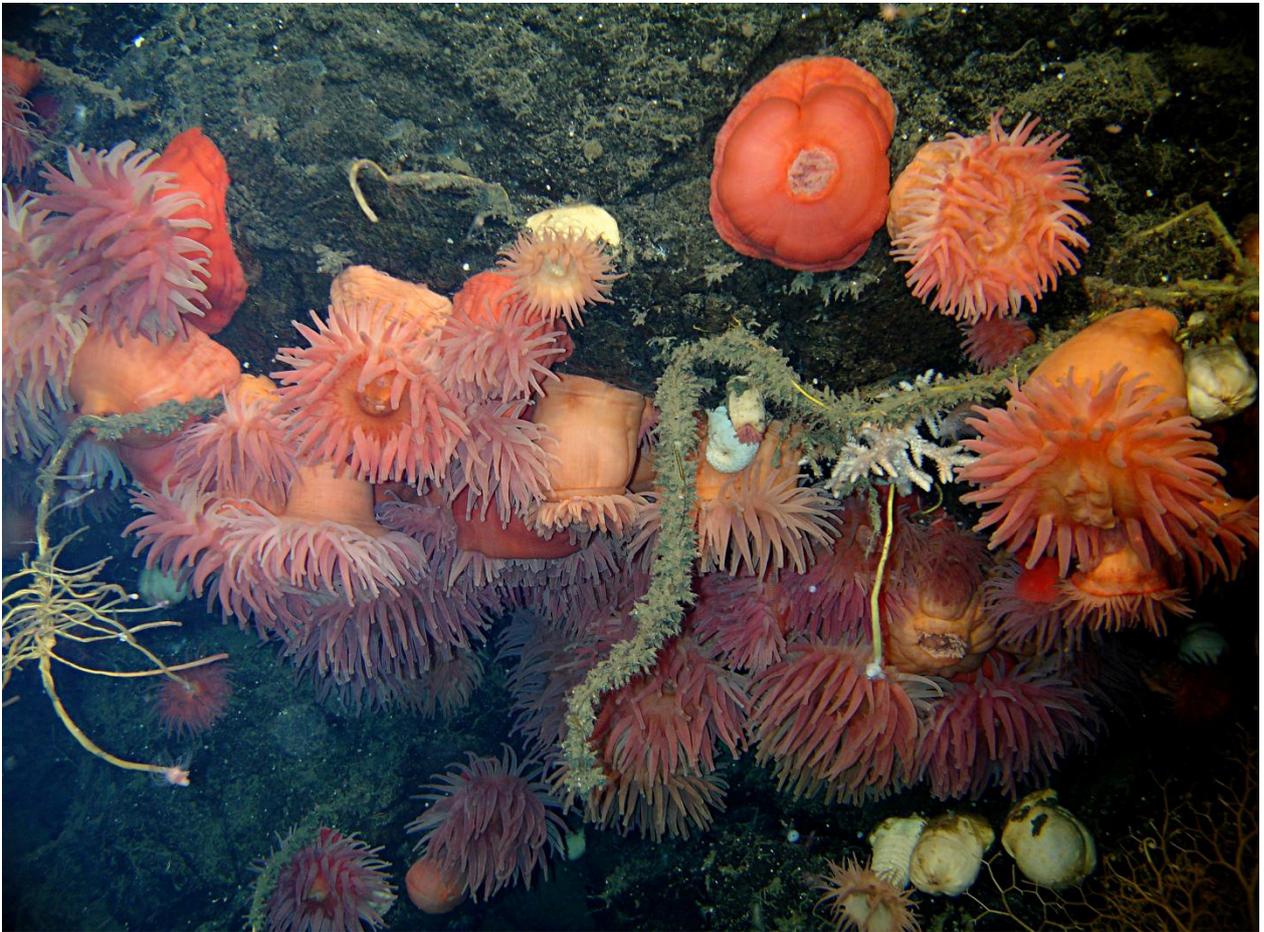




Symposium Program and Book of Abstracts



12th International Deep-Sea Biology Symposium
Reykjavík, Iceland
7-11 June, 2010

Hosted by the University of Iceland

Symposium Program and Book of Abstracts

Organizing committee:

Jörundur Svavarsson, chair

Halldór Pálmar Halldórsson

Sigurður Þórðarson

Eric dos Santos

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**12th International Deep-sea Biology Symposium, 7-11 June 2010,
Askja – Natural Science Building, Reykjavík, Iceland**

Welcome

The deep-sea is among the most spectacular and fascinating environments of our planet and yet, it is also among the most poorly explored habitats in the world. The international deep-sea symposia have been invaluable platforms for exchange of information concerning this remarkable environment and of deep-sea research in general. Furthermore, the deep-sea symposia have been an active well-spring for co-operation, new projects and the formation of research groups. Numerous offers of berth at sea have been given during these symposia in the past. For some of us, the early deep-sea meetings and later the full scale deep-sea symposia in Stockholm (1977), Kristineberg (1977), La Jolla (1981), Hamburg (1985), Brest (1988), Copenhagen (1991), Heraklion (1994), Monterey Bay (1997), Galway (2000), Coos Bay (2003) and Southampton (2006) mark the highlights of deep-sea exploration. Holding the symposium in Iceland is therefore a great honour for Iceland and the University of Iceland as it shows we are trusted to host this great event and to receive you all as our guests.

The planning of the symposium in Iceland has been under the shadow of a high plume of ash coming from the volcano under the glacier of Eyjafjallajökull. The volcanic activity, warm springs emerging from the earth and many other characteristics of our beautiful country bear a close resemblance to many of the spectacular phenomena of the deep-sea environment, such as the hydrothermal vents. During our excursion we hope to be able to compare these extreme environments, i.e. the deep-sea and Iceland!

Welcome to Iceland! We hope that we will all have a splendid time, both during the scientific sessions and through the social events. We wish to thank the Minister of Education, Science and Culture, the Rector of the University of Iceland, and the Town Council of Sandgerði for their support and help in making this symposium possible.

The organizing committee of the 12thDSBS

Jörundur Svavarsson, chair

Sigurður Þórðarson

Halldór P. Halldórsson

Eric dos Santos

PROGRAMME OF ORAL PRESENTATIONS

Sunday 6th June

17.00 Registration begins at Askja, Natural Science Building

22.00 Registration ends

Monday 7th June

08.00 **Registration continues at Háskólabíó (The University cinema)**

08.55 **Opening ceremony in Hall no. 1 at Háskólabíó (The University cinema)**

08.55 Jörundur Svavarsson, chair of the organizing committee Welcome

09.00 Katrín Jakobsdóttir, Minister of Education, Science and Culture Addressing the conference

09.10 Kristín Ingólfssdóttir, Rektor, University of Iceland Addressing the conference

Diverse aspects of the deep-sea

09.20 Young C.M., Smart T., Bennett K., Wolf M. and Emlet R.B. Does ecological release from predators permit slow development and extended planktonic periods in deep-sea embryos and larvae?

09.40 Witte U., Burke K. and Jeffreys R. Climate change, pelagic-benthic coupling and deep-sea ecosystem functioning

10.00 Jacobsen K. and Van Dover C. Beyond the edge of the sea; diversity of life in the deep ocean wilderness – a traveling exhibit merging the art with the science of the deep sea, featuring the illustration work of Karen Jacobsen, and the scientific expertise of Dr. Cindy Van Dover

10.20 **Tea and Coffee**

Diverse aspects of the deep-sea – continued

10.40 Sibuet M., Carney R. and Menot L. and COMARGE members Continental Margin Biodiversity

11.00 Morris K.J., Tyler P.A. and Rogers A.D. Distribution and abundance of deep-sea corals upon an Axial Volcanic Ridge (AVR) of the Mid-Atlantic Ridge at approximately 45°W 30' N

- 11.20 Wishner K.F. Zooplankton in the eastern Tropical North Pacific oxygen minimum zone
- 11.40 Etter R., Boyle E., Glazier A., Dutra E., Chase M. and Jennings R. Evolution in the deep Atlantic inferred from the phylogeography of an abyssal protobranch bivalve
- 12.00 Thornhill D.J., Hatleberg W., Fielman K.T., Santos S.R. and Halanych K.M. Recent insights on siboglinid phylogeny, symbiosis and evolution
- 12.20 **Lunch at Háskólabíó (The University cinema)**

Monday 7th June
Parallel session #1
Lecture hall 132, Askja:

Hydrothermal cold seepssystem and organisms

Chair: Joëlle Galéron, Ken Halanych

- 13.20 Cuvelier D., Sarrazin J., Colaço A., Copley J.T., Desbruyères D., Glover A., Tyler P.A. and Serrão Santos R. 14 years of community dynamics at the Atlantic Eiffel Tower hydrothermal edifice
- 13.40 Burgaud G., Arzur D., Durand L., Cambon-Bonavita M.A., Birrien J.L. and Barbier G. Fungal communities in deep-sea hydrothermal ecosystems
- 14.00 Cambon-Bonavita M.-A., Durand L., Cueff-Gauchard V., Dupéron S., Roussel E., Guri M., Shillito B. and Zbinden M. New insights on the diversity among microbial communities associated to the hydrothermal shrimp *Rimicaris exoculata*: a double symbiosis.
- 14.20 Génio L., Hilário A., Nolasco R., Dubert J. and Cunha M.R. Amphi-Atlantic chemosymbiotic mussel species "*Bathymodiolus*" *mauritanicus*: insights into larval dispersal using physical modeling
- 14.40 Goroslavskaya E. Composition and structure of mytilid-based assemblages on hydrothermal fields in the Atlantic and Pacific Oceans
- 15.00 St Germain C. and Tunnicliffe V. Population connectivity in a biostructuring hydrothermal vent tubeworm
- 15.20 **Tea, coffee and posters**

Hydrothermal cold seep system and organisms – continued

Chair: Joëlle Galéron, Ken Halanych

- 15.40 Lunina A.A. Phylogenetic analysis of the vent shrimps and geographic distribution of the clades
- 16.00 Watanabe H., Reynolds K., Sasaki T., Uematsu K., Strong E., Miyake H., Suzuki Y., Kojima S., Kim S., Young C. and Fujikura K. Novel ciliated larval form, unique brooding, and early release of vent gastropod *Ifremeria nautilei*
- 16.20 Carney R., Ziebis W., Bertics V. and Chow C.-E. A report at year 6 for long-term colonization of artificial sulfidic substrate by chemosynthetic fauna
- 16.40 De Groote A. and Vanreusel A. Meiofauna of deep-sea cold seeps in the Eastern Mediterranean area, with special emphasis on nematode biodiversity and connectivity
- 17.00 Forget N.L. and Juniper S.K. A comparison of bacterial diversity in two contrasting tubeworm habitats

18.15 Excursion to Sandgerði - Icebreaker and Reception

Monday 7th June

Parallel session #2

Lecture hall 131, Askja:

Corals, coral reefs and associated organisms

Chair: Scott France, Christoffer Schander

- 13.20 Hourigan T., Clarke M.E., David A., Dorfman D., Sullivan M. and Tsao F. The Deep Sea Coral Research and Technology Program: research to conserve biodiverse deep-sea ecosystems
- 13.40 Gheerardyn H., Raes M., De Troch M., Vincx M. and Vanreusel A. Meiofauna associated with cold-water corals: composition, diversity and adaptation
- 14.00 Baker K.D., Haedrich R.L., Gilkinson K., Wareham V.E., Edinger E.N. and Snelgrove P.V.R. Deep-sea fishes and coral habitat associations on the Grand Banks, Newfoundland
- 14.20 Van Oevelen D., Duineveld G., Lavaleye M., Mienis F., Soetaert K., Hoytema N. and Heip C. The cold-water coral community as a hotspot of carbon cycling on continental margins: a food web analysis from Rockall Bank (northeast Atlantic)

- 14.40 Marshall C., Howell K., Glegg G., Jacobs C. and Stewart H. The devil is in the detail: ecological insight and management implications differ after modelling deep sea gorgonian distribution using different data resolutions
- 15.00 Pante E., France S.C., Watling L. and Samadi S. Insights into the evolution and biogeography of chrysogorgiid corals

15.20 **Tea, coffee and posters**

Corals, coral reefs and associated organisms – continued

Chair: Scott France, Christoffer Schander

- 15.40 Watling L., France S.C., Pante E. and Thoma J. Atlantic - Pacific relationships of deep-sea octocorals
- 16.00 Beazley L. and Kenchington E. Reproductive biology of the cold-water coral *Acanella arbuscula*, Northwest Atlantic
- 16.20 Sun Z., Hamel J.-F. and Mercier A. Planulation patterns, larval development, settlement and early growth of deep-sea octocorals from the northwest Atlantic
- 16.40 Falkenhaug T. and Sudnik S. Reproductive patterns in pelagic decapod shrimps from the Northern Mid-Atlantic Ridge

18.15 Excursion to Sandgerði - Icebreaker and Reception

Tuesday 8th June
Parallel session #1
Lecture hall 132, Askja:

Hydrothermal and cold seep – continued

Chair: Lisa Levin, Alexander Vereshchaka

- 9.00 Galéron J., Olu K., Fifis A., Crassous P., Menot L., Gauthier O. and Voisset M. Spatial heterogeneity of megafaunal communities related to fluid seepage in the Niger delta
- 9.20 Levin L. A., Orphan B., Rouse G., Rathburn A., Grupe B., Mendoza G., Thurber A., Hutzler A., Jellison B. and Waren A. The Carbonate Nation: ecosystem engineering by carbonate-precipitating microbes at Costa Rica methane seeps
- 9.40 Ritt B., Gauthier O., Caprais J.-C., Olu K. and Sarrazin J. Composition and spatial patterns of cold seep communities from different geological structures in the deep eastern Mediterranean Sea
- 10.00 Thurber A., Jones W.J. and Schnabel K. Dancing for food in the deep-sea: a unique symbiosis by a novel species of yeti crab
- 10.20 **Tea, coffee and posters**

Hydrothermal and cold seep - continued

Chair: Lisa Levin, Alexander Vereshchaka

- 10.40 Colaço A., Cordeiro N., Cunha M., Gaudron S.M., Lino S., Nunes Jorge A., Rodrigues C. and Serrão Santos R. Trophic structure of colonization modules at chemosynthetic environments: a comparative approach
- 11.00 Duperron S. An overview of deep-sea mussel symbioses: facts, hypotheses and future directions
- 11.20 Gaudron S.M., Cunha M.R., Fardeau M.L., Ollivier B., Le Bris N., Colaço A., Henriot J.-P., Boetius A., Barbier G., Guillou L., Gros O., Pierre C., Duperron S., Wenzhöfer F., Borowski C., Burgaud G., Rodrigues C., Sauvadet A.-L., Hilário A. and Gaill F. CHEMECO (Colonization processes in CHEMosynthetic ECOsystems) Eurodeep ESF: a synthesis
- 11.40 Rodrigues C.F., Brissac T., Halary S., Boetius A., Cunha M.R., Gaudron S.M. and Duperron S. Looking at some chemosynthetic species: from Atlantic to Eastern Mediterranean

12.00 Lunina A.A. and Vereshchaka A.L. Life cycle of *Rimicaris exoculata* above the North-Atlantic Ridge

12.20 Offers of sites for the 13th DSBS

12.30 **Lunch at Askja**

Biodiversity

Chair: Eric dos Santos, Ann Vanreusel

13.20 Ruhl H.A., Hughes S.J., Boorman B., Alt C., Ross E. and Billett D.S.M. Long-term variation in biodiversity and ecosystem function of abyssal megafauna

13.40 Cunha M.R., Génio L., Hilário A., Moura C.J., Ravara A. and Rodrigues C.F. Is the Gulf of Cadiz a biodiversity hotspot in the NE Atlantic?

14.00 Ingels J., Kiriakoulakis K., Wolff G.A., Billett D.S.M. and Vanreusel A. The impact of deep-sea canyon conditions on meiobenthic structure and function

14.20 Hasemann C., Sablotny B. and Soltwedel T. Impact of macrofauna bioturbation on small-scale distribution patterns of deep-sea meiofauna: An experimental approach

14.40 Tecchio S., Ramírez-Llodra E., Sardà F., Company J.B. and Mechó A. Megabenthos diversity patterns in the deep Mediterranean along depth and west-to-east axes

15.00 Pape E., Moodley L. and Vanreusel A. Meiofaunal biodiversity and ecosystem functioning at the Galicia Bank (NE-Atlantic)

15.20 **Tea, coffee and posters**

Biodiversity – continued

Chair: Eric dos Santos, Ann Vanreusel

15.40 McClain C.R. and Barry J.P. Habitat heterogeneity, biogenic disturbance, and resource availability work in concert to regulate biodiversity in deep submarine canyons

16.00 Mamouridis V., Cartes J., Parra S., Fanelli E. and Saiz S.J.I. A temporal analysis on the dynamics of deep-sea macrofauna: influence of environmental variability off Catalonia coasts (western Mediterranean).

16.20 Linse K., Brandt A. and Enderlein P. Diversity of Antarctic deep-water bivalves – with special references their macrobenthic assemblages in the Atlantic Sector of the Southern Ocean

- 16.40 Corbari L., Compère P.,
Trevisan M., Boisselier M.C.,
Samadi S. and
Richer de Forges B. Biodiversity of sunken wood associated
crustaceans (Amphipoda, Isopoda)
- 17.00 Kamenskaya O., Gooday A.J.,
Radziejewska T., Melnik V.
and Wawrzyniak-Wydrowska
B. Little-known large protists (Komokiacea and
Xenophyophorea) in the macrobenthos of an
abyssal polymetallic nodule field
- 17.20 Paterson G., Soto E., Billett D.,
Galeron J., Sibuet M. and
Hawkins L. Temporal variability in polychaete
assemblages of the abyssal NE Atlantic
Ocean: the species response
- 17.40 Kupriyanova E.K. Undiscovered diversity of deep-sea serpulid
polychaetes
- 18.00
to **Late poster session in Askja and shark tasting offered by Star-Oddi**
20.00

Tuesday 8th June
Parallel session #2
Lecture hall 131, Askja:

The deep pelagic

Chair: Tone Falkenhaus, Halldór P. Halldórsson

- 9.00 Haddock S.H.D. and Thuesen
E.V. Temporal and spatial dynamics of
mesopelagic macroplankton
- 9.20 Heino M., Falkenhaus T.,
Piatkowski U., Porteiro F.M.
and Sutton T.T. Depth-abundance and depth-size relationships
for deep-living nekton in the mid North
Atlantic
- 9.40 Boersch-Supan P.H., Read J.F.,
Rogers A.D. and Brierley A. Distribution of epi- and mesopelagic
scattering layers around Indian Ocean seamou
- 10.00 Matabos M., Aguzzi J., Robert
K., Costa C., Menesatti P.,
Company J.B., Tunnicliffe V.
and Juniper S.K. A preliminary multi-parametric study on
behavioural modulation in demersal decapods
of Saanich Inlet by VENUS platform
- 10.20 **Tea, coffee and posters**

The deep pelagic – continued

Chair: Tone Falkenhaus, Halldór P. Halldórsson

- 10.40 Lindsay D.J., Fuentes V., Bentlage B., Collins A., Toda R., Hopcroft R. and Kirby R. Frozen jelly in the blender: ubiquitous species, endemic species, and biodiversity in the gelatinous plankton community of Eastern Antarctica
- 11.00 Kulagin D. Vertical distribution of chaetognaths in the Drake Passage
- 11.20 Stupnikova A. Dominant species of the genus *Calanus* in the North Atlantic: species range limits significantly moved to South
- 11.40 Mackey A.P. and Cunningham N.J.J. Extending our knowledge into the past: the rescue and reanalysis of historic zooplankton catch data from the Discovery investigations 1925-1951
- 12.00 Jeffreys R., Lavaleye M., Bergman M., Duineveld G., Witbaard R. and Linley T. Reconciling the link between deep-sea fish and surface water production: evidence from in situ observations.
- 12.20 Offers of sites for the 13th DSBS
- 12.30 **Lunch at Askja**

Deep-sea fish

Chair: Odd Aksel Bergstad, Michael Vecchione

- 13.20 Bailey D.M., Brown S., Godbold J.A., King N.J., Priede I.G., Collins M.A. and Gordon J.D.M. Long-term change in structure of the deep-water fish community of the Porcupine Seabight and Abyssal Plain
- 13.40 Catarino D., Menezes G. and Stefanni S. Fishing deep: longline surveys in mid-Atlantic seamounts
- 14.00 Cook A., Sutton T., Galbraith J. and Vecchione M. Deep-pelagic (0-3000 m) fish assemblage structure over the Mid-Atlantic Ridge relative to the North Atlantic subpolar front
- 14.20 Schneider M. The benthic fish fauna of abyssal plains in the Southern Atlantic
- 14.40 Hunter R.C. Age and growth of macrourid fishes from the mid-Atlantic Ridge

- 15.00 Fernandez-Arcaya U., Recasens L., Ramirez-Llodra E., Rotllant G., Cerviño C., Bruno M. and Company J.B. Distribution and reproductive biology of deep-sea grenadier fish (Family: Macrouridae) from the northwestern Mediterranean Sea
- 15.20 **Tea, coffee and posters**
- Deep-sea fish – continued*
Chair: Odd Aksel Bergstad, Michael Vecchione
- 15.40 Trenkel V.M. and Lorance P. Estimating *Synaphobranchus kaupi* densities: contribution of fish behaviour to differences between baited camera and strip transects
- 16.00 Carmo V., Menezes G., Bergstad O. A. and Sutton T. Feeding of stomiiform fishes of the northern Mid-Atlantic Ridge
- 16.20 Knutsen H., Jorde P.E., Skogen M. and Bergstad O.A. Population structure in the deep sea fish, roundnose grenadier (*Coryphaenoides rupestris*), as revealed by microsatellite DNA
- 16.40 Dunn M. Orange roughy fisheries around New Zealand; the first and last?
- 17.00 Bergstad O.A., Øverbø Hansen H. and Jørgensen T. Temporal variation in abundance, recruitment and distribution of a commercially exploited deepwater fish, the roundnose grenadier *Coryphaenoides rupestris*
- 17.20 Reid W.D.K., Wigham B.D., Polunin N.V.C., Sweeting C.J. and McGill R.A. Spatial variability in size-related shifts in deep-sea fish trophodynamics elucidated by stable isotopes
- 17.40 Vecchione M. The cirrate-octopod assemblage of the Charlie-Gibbs Fracture Zone, Mid-Atlantic Ridge
- 18.00
to **Late poster session in Askja and shark tasting offered by Star-Oddi**
20.00

Wednesday 9th June

**A full day excursion to Thorsmörk or Landmannalaugar
(departure at 08.00 from Askja, the symposium venue)**

Thursday 10th June
Parallel session #1
Lecture hall 132, Askja:

Biodiversity – continued

Chair: Jeff Drazen, Emanuella Fanelli

- 9.00 Bik, H.M., Sung, W. and Thomas W.K.T. Metagenetic analysis of biodiversity patterns in deep-sea benthic meiofaunal communities
- 9.20 Méndez N. Collection and quantification of deep-sea macrobenthos: a case study of the polychaete *Melinnampharete gracilis*
- 9.40 Tittensor D.P., Schlacher T., Smith C.R. and Susko E. Endemism at low sampling effort: real or artifact?
- 10.00 Yasuhara M., Hunt G., Cronin T. M. and Okahashi H. Temporal latitudinal-gradient dynamics and tropical instability of deep-sea species diversity for the last 500,000 years
- 10.20 **Tea, coffee and posters**

Biodiversity - planktonic/trophic

Chair: Jeff Drazen, Emanuella Fanelli

- 10.40 O'Hara T.D. Biogeographic analyses of deep-sea fauna using species habitat models
- 11.00 Letessier T B, Cox M.J., Pond D.A., McGill R. and Brierley A.S. Pelagic zooplanktic trophic structure over the Charlie Gibbs fracture zone/subpolar front of the Mid-Atlantic ridge: a stable isotope and fatty acid analysis approach.
- 11.20 Choy C.A., Popp B.N. and Drazen J.C. Pelagic food web connectivity in the Central North Pacific Ocean with a focus on deep ocean mid-trophic level groups
- 11.40 Fanelli E., Cartes J. and Papiol V. Trophodynamics of deep-sea macrozooplankton and micronekton off the Catalan slope: insight from stable isotopes
- 12.00 Wilson S.E. and Smith K.L. Feeding ecology of meso- and bathypelagic zooplankton as indicated by scanning electron microscopy of fecal pellets from live animals and sediment trap samples
- 12.20 **Lunch at Askja**

Food webs

Chair: Ursula Witte, Bhavani Narayanaswamy

- 13.20 Gontikaki E., van Oevelen D., Soetaert K. and Witte U. Benthic food web interactions in the deep Faroe-Shetland Channel: combining stable isotope labelling with linear inverse modelling techniques
- 13.40 Enge A., Nomaki H., Ogawa N. O., Lavik G., Witte U., Moeseneder M.M., Ohkouchi N., Kitazato H., Kucera M. and Heinz P. Species-specific carbon uptake by an abyssal foraminiferal community during a simulated phytodetrital pulse in the North Pacific
- 14.00 Guilini K., Van Oevelen D., Soetaert K., Middelburg J.J., Soltwedel T., Moens T. and Vanreusel A. The trophic ecology and colonization capacity of deep-sea nematodes: experimental evidence
- 14.20 Mayor D.J., Thornton B., Hay S. and Witte U. Food quality and season affect carbon cycling in deep sea sediments
- 14.40 Moeseneder M., Prosser J., Smith K. and Witte U. DNA-SIP analysis reveals rapid response of abyssal bacterial and crenarchaeal communities to phytodetritus deposition
- 15.00 Nomaki H., Ogawa N., Takano Y., Suga H., Ohkouchi N., Toyofuku T. and Kitazato H. Utilization of dissolved organic matter by the deep-sea benthic community at the Sagami Bay, Japan
- 15.20 **Tea, coffee and posters**

Food webs - benthic communities

Chair: Ursula Witte, Bhavani Narayanaswamy

- 15.40 Pozzato L., Moodley L., Soetaert K. and Middelburg J.J. Biodiversity, trophic linkages and carbon flow in the deep-sea benthic food-web
- 16.00 Amaro T., Danovaro R., Billett D.S.M. and Cunha M.R. Ecosystem functioning in the deep sea: the trophic biology of the holothurian *Molpadia musculus* at 3,500 m in the Nazaré Canyon, Portuguese Margin
- 16.20 Itoh M., Kawamura K., Kitahashi T., Kojima S. and Shimanaga M. Bathymetric patterns of meiofaunal standing stocks associated with the Kuril and Ryukyu trenches, western North Pacific Ocean

- 16.40 Janussen D. and Göcke C. Porifera (Sponges) of the deep Weddell Sea, Antarctic: Preliminary results from the ANDEEP-SYSTCO expeditions, 2002-2008 with RV "Polarstern"
- 17.00 Narayanaswamy B.E. and Bett B.J. Biomass relations in the Faroe-Shetland Channel: an Arctic-Atlantic boundary environment
- 19.00 **Symposium dinner at Radisson Hotel Blue, Saga Hotel (Súlnasalur)**

Thursday 10th June
Parallel session #2
Lecture hall 131, Askja:

Environmental aspects

Chair: Kerry Howell, David Thistle

- 9.00 Sedlacek L., Thistle D., Carman K. R., Fleeger J.W. and Barry J. P. Effects of carbon dioxide on deep-sea harpacticoids revisited
- 9.20 Swaddling A. and Smith S. Environmental conditions at a deep sea site proposed for commercial development: Solwara 1, Papua New Guinea
- 9.40 Smith S. Unlocking mineral resources from the deep seafloor: environmental considerations
- 10.00 Howell K., Davies J., Golding N., Jacobs C., Narayanaswamy B. and Stewart H. Mapping the deep - the UK's deep-sea marine protected area network project
- 10.20 **Tea, coffee and posters**

Environmental aspects – continued

Chair: Kerry Howell, David Thistle

- 10.40 Rogers A.D. Protection of deep-sea ecosystems by regional fisheries management organisations (RFMOs)
- 11.00 Benn A.R., Weaver P.P., Billett D.S.M., van den Hove S., Le Bas T., Murdock A. and Doneghan G. A quantitative assessment of anthropogenic activities in the deep North East Atlantic

- 11.20 Clark M., Williams A., Rowden A., Althaus F., Baco A., Schlacher T., Tittensor D., Consalvey M. and Bowden D. The impacts of human activities on seamounts: low resilience of faunal communities to trawling and mining
- 11.40 Koenig S, Company J.B., Fernandez P. and Solé M. Do organic contaminants accumulate more in submarine canyons than along the open slope? A case study of Blanes canyon, NW Mediterranean
- 12.00 Barry J.P., Buck K.R., Pane E.R., Lovera C., Whaling P.J. and Tanner C. Effects of ocean acidification on metabolism and acid-base balance in brachiopods (*Laqueus californianus*): implications for the fossil record and the future
- 12.20 **Lunch at Askja**
- Molecular genetics***
Chair: Sigurður Þórðarson, Saskia Brix
- 13.20 Lejzerowicz F. and Pawlowski J. Recovery of eukaryotic DNA from downcore deep-sea samples
- 13.40 Quattrini A.M., Etnoyer P. and Cordes E. Phylogenetic diversity of octocorals in the Gulf of Mexico
- 14.00 Reveillaud J., van Soest R., Derycke S., Erpenbeck D., Cárdenas P., Xavier J., Picton B., Rigaux A. and Vanreusel A. Plans to protect deep-water coral ecosystems along the European margins: new insights from phylogenetic analyses of the associated Porifera
- 14.20 Sinniger F. and Baco A. Investigations of the diversity and substrate specificity of Pacific seamount zoanthids
- 14.40 Taylor M.L., Agnew D.J., Cairns S.D. and Rogers A.D. Using DNA taxonomy to estimate octocoral diversity: the search for octocoral's silver-bullet(s)
- 15.00 Thubaut J., Lorion J., Corbari L., Duperron S., Gros O. and Samadi S. Integrative biology of a 'model species', *Adipicola iwaotakii*, associated with sunken organic substrates
- 15.20 **Tea, coffee and posters**

Molecular genetics– continued

Chair: Sigurður Þórðarson, Saskia Brix

- 15.40 Plouviez S. and Jollivet D. Multigene analysis of polymorphism versus divergence reveals allopatric speciation processes and demographical expansion along the East Pacific Rise
- 16.00 Brix S. A comparison of neighbouring deep-sea basins. High genetic distances in species of the genus *Chelator* Hessler, 1970 (Isopoda: Desmosomatidae)?
- 16.20 Stefanni S., Bettencourt R., Pinheiro M. and Egas C. Sequencing and analysis of a multiple tissue-specific transcriptome from the black scabbardfish, *Aphanopus carbo* (Perciformes: Trachiuroidae) using 454 technology
- 16.40 Hall S., Thatje S. and Held C. The evolutionary history and phylogeny of the sub-family Lithodinae (Decapoda: Anomura: Lithodidae)
- 17.00 Sigwart J.D. and Yearsley J.M. Larval transport modelling of deep-sea invertebrates points to potential undiscovered populations
- 19.00 **Symposium dinner at Radisson Hotel Blue, Saga Hotel (Súlnasalur)**

Friday 11th June
Parallel session #1
Lecture hall 132, Askja:

Food webs - benthic communities

Chair: Sigurður Þórðarson

- 9.00 Buhl-Mortensen L. and Buhl-Mortensen P. Depth zonation of deep-sea benthos on the margin of the Norwegian Sea – Results from MAREANO
- 9.20 Srsen P., Smith C.R. and Altamira I. Variations in benthic community structure, abundance and diversity along an antarctic latitudinal sea ice gradient
- 9.40 De Leo F., Smith C., Rowden A., Bowden D. and Clark M. Kaikoura submarine canyon, East New Zealand margin: an oasis of food for deep-sea benthic communities
- 10.00 Hunter W.R., Moeseneder M. and Witte U. Organic matter turnover in the Arabian Sea oxygen minimum zone: the role of oxygen availability and benthic community structure
- 10.20 **Tea, coffee and posters**

Benthic communities – continued

Chair: Sigurður Þórðarson

- 10.40 Sherman A. D., McGill P.R., Henthorn R.G., Hobson B.W. and Smith, K.L.Jr. Long time-series measurements of benthic community processes to abyssal depths using an autonomous bottom-transiting vehicle
- 11.00 Radziejewska T., Beaulieu S.E., Kaufmann R.S. and Smith K.L.Jr. Life under glass houses: the impact of glass sponges on meiofaunal abundance in sediments at abyssal depth in the NE Pacific
- 11.20 Smith C. R., Grange L. and Clark C. E. High megabenthic abundance and diversity in deep fjords of the West Antarctic Peninsula: high sensitivity to climate change?
- 11.40 Soltwedel T., Bergmann M., Hasemann C., Kanzog C., Lochthofen N., Sauter E. and Schewe I. Dropstones: sources for habitat heterogeneity in the deep Arctic Ocean

- 12.00 Syranidou E., Lampadariou N., Tselepides A. and Smith, K.L.Jr Deep-sea meiofauna communities and associated biogenic structures in the NE Pacific
- 12.20 **Lunch at Askja**
- Benthic communities – continued*
Chair: Eric dos Santos, Charles G. Messing
- 13.20 Menot L., Carlier A., Galéron J., Grall J., Olu K. and Sarrazin J. Influences of hotspots (canyon, coral reef, mud volcanoes) on macrobenthic communities in the deep Mediterranean Sea
- 13.40 Moodley L., Nigam R., Ingole B., Prakash Babu C., Middelburg J.J., Soetaert K. and Heip C.H.R. Oxygen minimum seafloor ecological (mal) functioning
- 14.00 Ross E., Bett B., Billett D., Henson S., Iglesias-Rodriguez D., Rogacheva A., Ruhl H., Tyler P. and Huvenne V. Satellite to seafloor: ocean colour and holothurian distribution
- 14.20 Lorance P., Dransfeld L., Barrio Froján C.S.R., Kenny A.J., Large P.A. and Trenkel V.M. Environmental assessment of the deep-water ecosystem to the west of the British Isles
- 14.40 Messing C., Reed J., Brooke S. and Richardson S. A possible role for agglutinated foraminiferans in the development of deep-water coral mounds
- 15.00 Kalogeropoulou V., Billett D.S.M., Gooday A.J., Lampadariou N., Martinez Arbizu P., Tselepides A. and Vanreusel A. Temporal changes, during a fifteen-year period (1989-2004), in deep sea metazoan meiofaunal assemblages at the Porcupine Abyssal Plain, NE Atlantic
- 15.20 **Tea, coffee and posters**
- Benthic communities – continued*
Chair: Eric dos Santos, Charles G. Messing
- 15.40 Schewe I., Freese D., Soltwedel T. and Klages M. Recolonization of experimental deployed sediments by meiobenthos organisms in an arctic deep-sea environment
- 16.00 McCarthy D.M., Gill A., Patching J.W. and Gerard T.A. Distribution and community structure of ultramicrobacteria in the Mediterranean Sea
- 16.20 Bergmann M., Ontrup J., Nattkemper T.W., Soltwedel T. and Klages M. Longer-term dynamics of megafaunal assemblages from the Arctic observatory HAUSGARTEN (eastern Fram Strait, 79°N)

- 16.40 Baco A., Kelley C., Rowden A. and Clark C. A comparison of the fauna of cobalt-rich and non cobalt-rich seamounts
- 17.00 Davies J.S., Howell K.L., Jacobs C., Narayanaswamy B., Stewart H. and Golding N. Mapping the benthic assemblages of Anton Dohrn Seamount
- 17.20 Rowden A.A., Schlacher T.A., Dower J.F., Consalvey M., Clark M.R., O'Hara T.D. and Stocks K.I. A synthesis of seamount ecological paradigms: fact, fiction and the future
- 17.40 ***Closing ceremony in Lecture hall 132***

Friday 11th June
Parallel session #2
Lecture hall 131, Askja:

Whale falls and other peculiar things

Chair: Halldór P. Halldórsson, Kirsty Kemp

- 9.00 Aguzzi J., Furushima Y., Chiesa J.J., Costa C., Menesatti P., Fujiwara Y. and Company J.B. Behavioural rhythms in deep-water continental margins and the deep-sea
- 9.20 Colmenero A. I., Aguzzi J., Bozzano A. and Lombarte A. Sensory constraints in temporal segregation in two species of anglerfish (*Lophius budegassa* and *L. piscatorius*)
- 9.40 Glover A.G., Smith C.R., Wiklund H., Higgs N., Baco-Taylor A., Kemp K., Jamieson A., Little C.T.S. and Dahlgren T.G. New discoveries of whale-fall fauna from deep water off Antarctica and Southern California
- 10.00 Schlining K.L., Lundsten L., Frasier K., Johnson S.B., Kuhn L.A., Harvey J.B.J., Clague G. and Vrijenhoek R.C. Whale-fall community dynamics in Monterey Canyon, California, USA
- 10.20 **Tea, coffee and posters**

Ecology

Chair: Halldór P. Halldórsson, Kirsty Kemp

- 10.40 Verna C., Ramette A., Wiklund H., Dahlgren T.G., Glover A.G., Gaill F. and Dubilier N. Comparative symbiont diversity in the bone-eating worm *Osedax* from shallow and deep-sea whale-falls
- 11.00 Johnson S.B., Waren A., Lee R.W., Kano Y, Kaim A, Davis A., Strong E.E. and Vrijenhoek R.C. Living fossils? New/old bone-eating snails from the deep-sea
- 11.20 Yeh J. and Drazen J. Megafaunal scavenger ecology of the Californian slope
- 11.40 Sardà F. and Company J.B. Recruitment of deep-sea rose shrimp *Aristeus antennatus* (Risso, 1816) on Mediterranean bathyal habitats
- 12.00 Dahlgren T.G. and Glover A.G. On wood in the Antarctic, and the fate of shipwrecks
- 12.20 **Lunch at Askja**

Physiology

Chair: Halldór P. Halldórsson, Sven Thatje

- 13.20 Hoving H.J.T. Mating tactics in deep-sea squid
- 13.40 Brown A. and Thatje S. Respiratory response of the deep-sea lysianassoid amphipod *Stephonyx biscayensis* (Chevreux, 1908) to temperature and hydrostatic pressure
- 14.00 Cottin D., Shillito B., Chertemps T., Thatje S., Leger N. and Ravaux J. Thermal stress response of the hydrothermal vent shrimp *Rimicaris exoculata*
- 14.20 Drazen J. C., Yeh J., Condon N. and Friedman J. Metabolism of demersal fishes from the eastern North Pacific
- 14.40 Laxson C.J., Condon N., Drazen J.C. and Yancey P.H. Decreasing urea:methylamine ratios with depth in chondrichthyan fishes: a physiological depth limit?

15.00 Mestre N.C., Thatje T. and Tyler P.A. The ocean is not deep enough: pressure tolerances during early ontogeny of the blue mussel *Mytilus edulis*

15.20 **Tea, coffee and posters**

Physiology

Chair: Halldór P. Halldórsson, Sven Thatje

15.40 Oliphant A., Thatje S., Brown A., Morini M., Ravaux J. and Shillito B. Pressure tolerance of the shallow-water caridean shrimp, *Palaemonetes varians*, across its thermal tolerance window

16.00 De Busserolles F., Marshall N.J. and Collin S.P. Lanternfish vision: morphological measures of spatial resolving power and sensitivity

16.20 Thatje S. The role of specific dynamic action in the hydrostatic pressure tolerance of the shallow water spider crab *Maja brachydactyla*

16.40 Lord J., Burris Z., McNeill M. and Young C. Proximate effects of the egg-eating bivalve *Acesta oophaga* on the morphology and reproduction of its siboglinid tubeworm host

17.00 Billett D., Wolff G., Holtvoeth J., FitzGeorge-Balfour T., Fisher E., Bett B., Salter I., Boorman B., Hughes J., King N., Jamieson A., Bagley P. and Chaillan F. Benthic responses to natural iron fertilisation in the oceans

17.40 ***Closing ceremony in Lecture hall 132***

Poster Programme

Poster no.	Authors	Title
20	Addamo A.M., Taviani M. and Machordom A.	Molecular genetic characterization of <i>Desmophyllum dianthus</i> (Anthozoa, Hexacorallia) from the Mediterranean Sea: a preliminary study
66	Baczewska A., Błachowiak-Samołyk K. and Angel M.V.	Bathymetric and latitudinal gradients in the diversity of pelagic ostracods in the Central Eastern Atlantic Ocean
55	Baker M.C, Ramirez-Llodra E., Tyler P.A and German C.R.	The Census of Marine Life ChEss Programme - Global puzzle of deep-water chemosynthetic ecosystems: 8 years of discovery and investigation
67	Baldrighi E., Aliani S., Manini E. and Conversi A.	Small (≤ 10 km) spatial-scale variability in the distribution and biodiversity patterns of deep macrobenthic communities along the North-west Sardinia lobe: preliminary results
90	Barnes N., Glover A. and Ferrero T.J.	Diversity, dispersal and succession of whale-fall fauna in the deep sea
56	Bergstad O.A., Menezes G.M., Høines Å.S., Gordon J.D.M. and Galbraith J.	Patterns of distribution of deepwater demersal fishes of the North Atlantic mid-ocean ridge, continental slopes, islands and seamounts
91	Bernardino A.F. and Smith C.R.	Community structure of infaunal macrobenthos around vestimentiferan thickets at the San Clemente cold seep, NE Pacific
92	Bernardino A.F., Smith C.R., Baco A., Alyamira I. and Sumida P.Y.G.	Community structure in sediments around kelp and wood falls in the deep NE Pacific and species overlap with other reducing habitats
112	Bernhard J.M., Edgcomb V.P., Casciotti K.L., McIlvin M.R. and Beaudoin D.J.	Denitrification: not just for prokaryotes anymore?
105	Besteiro C., Moreira J., Urgorri V., Díaz-Agras G. and Candás M.	On some meiofauna from the Galician continental slope obtained during the campaign DIVA-Artabria 2009 on board R/V Sarmiento de Gamboa
68	Błazewicz-Paszkowycz M., Alvaro M. C., Davey N. and Schiaparelli S.	First evidence of parasitic behaviour in deep sea <i>Exspina typica</i> (Crustacea: Tanaidacea)

Poster no.	Authors	Title
69	Błażewicz-Paszkowycz M., Bamber R.N. and Cunha M.R.	Diversity of Tanaidacea (Crustacea) of European mud volcanoes
99	Boehnke R., Gluchowska M., Kwaśniewski S., Wojczulanis-Jakubas K., Walkusz W., Karnovsky N. and Błachowiak-Samołyk K.	The role of deep water zooplankters in feeding ecology of Little Auk – the matter of quality
1	Boyle E., Etter R. and Jennings R.	Phylogeny of the deep-sea protobranch subfamily, Ledellinae
113	Brault S., Stuart C.T., Wagstaff M. and Rex M.A.	Geographic evidence for source-sink dynamics in deep-sea gastropods: an approach using nested analysis
21	Brix S. and Riehl T.	DNA barcoding deep-sea Isopoda
114	Buck K., Walz K. and Barry J.	Biomass and metabolic partitioning amongst eukaryotic infauna from the bathyal deep-sea
2	Budaeva N.E. and Neretina T.V.	Revision of the deep-sea polychaete genus <i>Leptoecia</i> (Onuphidae) with description of a new species from the Mid-Atlantic Ridge
115	Buhl-Mortensen P., Buhl-Mortensen L. and Dolan M.	Characterisation of deep-sea habitats and biotopes within the MAREANO mapping area (Norwegian Sea/Barents Sea)
34	Campbell M.S. and Hall-Spencer J.M.	Distribution of cold-water corals around the UK and Ireland
116	Cartes J.E., Maynou F. and Fanelli E.	Nile damming as plausible cause of long-term changes in deep-sea Mediterranean communities over broad spatial scales
22	Catarino D., Stefanni S. and Menezes G.	Genetic diversity and length distribution of the offshore rockfish (<i>Pontinus kuhlii</i>) from three Atlantic archipelagos
35	Chavez K.M., Waller R. and Yancey P.H.	Organic osmolytes in deep-sea coral
33	Clark M.R., Watling L., Rowden A.A., Guinotte J.M. and Smith C.R.	A global seamount classification to aid the scientific design of marine protected area networks

Poster no.	Authors	Title
100	Colaço A., Giacomello E., Lombardi P., Martins A., Porteiro F., Serrão Santos R., Silva M., Tempera F. and Menezes G.	Trophodynamic studies of the CONDOR seamount (Azores, Portugal, North Atlantic)
46	Condon N.E., Friedman J.R. and Drazen J.C.	Metabolism and trophic levels of benthic and benthopelagic chondrichthyan fishes off the coast of California
29	Cook A.A.	The International Seabed Authority and marine scientific research
117	Cordes E., Hourdez S., Carney R. and Fisher C.	Examination of bathymetric patterns of deep-sea communities in a hydrocarbon-seep ecosystem
70	Cunha M.R., Paterson G.L.J., Amaro T., de Stigter H., Ferreira C., Glover A., Hilário A., Kiriakoulakis K., Neal L., Ravara A., Rodrigues C.F., Tiago A. and Billett D.S.M.	Diversity of macrofauna assemblages from three Portuguese submarine canyons (NE Atlantic)
47	De Leo F., Drazen J., Smith C. and Vetter E.	Quantitative assessment of deep-sea fish communities off Hawaii: the effect of submarine canyons and habitat structure on assemblage abundance and composition
48	De Leo F., Smith C. and Vetter E.	Enhanced macrofaunal abundance and beta diversity in three Hawaiian submarine canyons: deep-sea oases embedded in an oligotrophic ocean
57	Demina L. and Galkin V.	Trace metal bioaccumulation in mussel's and clam's shells at the deep-sea hydrothermal vent fields
86	Denda A. and Christiansen B.	Zooplankton at a seamount in the Eastern Mediterranean: distribution and trophic interactions
118	Díaz-Agras G., Aldea C., García-Álvarez O., Moreira J., Rodrigues M., Tato R., Troncoso J., Urgorri V. and Besteiro C.	Composition and distribution of the deep-sea benthic fauna off Western Galicia (NW Iberian Peninsula)

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108	Duffy G.A., Horton T., Shearer M. and Billett D.	Scavenging amphipods in deep-sea canyon ecosystems
49	Dunn M.	Quantifying the diet composition and guild structure of deep-sea fishes
58	Edgcomb V.P. and Bernhard J.M.	Ciliate-bacterial symbiosis: a cooperative strategy in low oxygen, sulfidic marine sediments?
71	Elsner N.O. and Brandt A.	Deep-sea isopod biodiversity and distribution in the Sea of Japan and the Kuril–Kamchatka area
101	Enderlein P. and Pond D.	Long term, deep water sediment trap moorings at contrasting productivity environments in the Southern Ocean, Antarctica
119	Esquete P., Falagán C., Somoza L., Moreira J. and Troncoso J.S.	Benthic macrofauna on methane-related features in the Gulf of Cádiz: preliminary results from MVSEIS08 cruise
3	Fernandez-Alamo M.A.	The occurrence of some mesopelagic, bathypelagic, and cold-water cosmopolitan species of holoplanktonic polychaetes in the Eastern Tropical Pacific Ocean
36	France S.C. and Watling L.	Deep-water octocorals of the Bahamas bathyal slope (Western North Atlantic) and their relationship to offshore seamount assemblages
83	Friedman J.R., Condon N.E. and Drazen J.C.	Metabolism and gill morphology of benthic fish species associated with the oxygen minimum zone within Monterey Bay, California
120	Galkin S.V., Gebruk A.V., Goroslavskaya E.I., Bergman M. and Soltwedel T.	Megabenthic community of the Håkon Mosby mud volcano: preliminary results of image analysis
4	Garcia-Alvarez O., Zamarró-Camino M., Urgorri V. and Señaris M.P.	Data about two new species of Mollusca Solenogastres from Antarctic Peninsula and Bellingshausen Sea (Bentart-2006 Expedition)

Poster no.	Authors	Title
72	García-Regueira X., Diaz-Agras G., Abad M., Moreira J. and Urgorri V.	Distribution of cumaceans (Crustacea, Peracarida) in the continental shelf and slope of Golfo Ártabro (Galicia, NW Iberian Peninsula)
30	Gates A. and Jones D.	Recovery of deep-water megafaunal assemblages from anthropogenic disturbance in the Norwegian Sea
5	Gheerardyn H. and Veit-Köhler G.	Large-scale biogeographical patterns of Paramesochridae in South Atlantic abyssal plains and the deep Southern Ocean: is the abyssal harpacticoid copepod fauna cosmopolitan?
73	Gill A., McCarthy D.M. and Fleming G.T.A.	Prokaryotic abundance and bacterial community structures in the deep Mediterranean Sea
59	Goroslavskaya E.	Composition and structure of vestimentiferan associated assemblages from Guaymas Basin and 9°N East-Pacific Rise: comparative analysis
60	Grupe B.M., Levin L.A., Hutzler A., Jellison B., Mendoza G.F., Rouse G.W., Thurber A.R. and Warén A.	Community composition and trophic patterns on rocks, wood, and biotic substrates at Costa Rican methane seeps
37	Guillaumont B. and Galéron J.	Cold-water corals of the Bay of Biscay: identification of species and habitats from video and still photographs
74	Göcke C. and Janussen D.	Bathymetric-zoogeographical traits of the Hexactinellida from the Antarctic deep-sea expeditions ANDEEP and SYSTCO
75	Hardy S.M., McClain C. and Smith C.R.	Sources and sinks in the abyss, and their consequences for deep-sea biodiversity
93	Higgs N.D., Little C.T.S., Dahlgren T.G., Fujiwara Y., Pradillon F., Smith C.R., Vrijenhoek R.C. and Glover A.G.	The diversity of <i>Osedax</i> (Annelida) borings revealed by computed tomography

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94	Hilario A., Colaço A. and Cunha M.R.	Colonization of mammal carcasses in the deep Atlantic Ocean: introducing the CARCACE project
109	Hunter R.C.	Reproductive ecology of deep-ocean fish
106	Ingels J., Tchesunov A.V., Popova E.V. and Vanreusel A.	Metazoan meiofauna in the Gollum Channel system and on the edge of the Whittard Canyon, Celtic Margin – how the environment shapes nematode structure and function, including notes on two new nematode species associated with ecto- and endosymbiotic prokaryotes
50	Jakobsdóttir K., Agnarsson S., Blanchard J., Cloete R., Diez G., Dransfeld L., Failler P., Figueiredo I., Gil-Herrera J., Gonzáles-Costas F., Large P. A, Planque B., Politou C.-Y. and Lorance P.	EU FP7 project DEEPFISHMAN Management and monitoring of deep-sea fishes and stocks
76	Jeffreys R., Lavaleye M., Bergman M., Duineveled G. and Baillon S.	Biodiversity and ecosystem functioning in the megabenthic community at Galicia Bank, Iberian margin
23	Jennings R.M., Ficara L., Shoshitaishvili B., Boyle E.E. and Etter R.J.	Strong genetic divergence along a bathymetric gradient - population divergence or cryptic speciation?
6	Kahn A.S., Geller J.B., Reisinger H.M. and Smith K.L. Jr	<i>Bathydorus laniger</i> and <i>Docosaccus punctata</i> (Lyssacinosa, Hexactinellida): two new species of glass sponges from the abyssal Northeast Pacific
38	Kemp K.M., Morris K.J., Yesson C. and Rogers A.D.	Investigation of cold water coral ecosystems of the Azores archipelago within the framework of EU FP7 project CoralFISH
95	Khelaifia S., Aussignargues C., Cayol J.-L., Cunha Ribeiro M., Gaudron S.M., Gaill F., Ollivier B. and Fardeau M.-L.	Isolation and characterization of sulfate reducing bacteria (SRB) from wood falls
7	Kihara T.C. and Martínez Arbizu P.	<i>Pontostratiotes</i> Brady, 1883 (Copepoda: Harpacticoida) from Angola deep-sea basin (Southeast Atlantic, DIVA 1)

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8	Kihara T.C. and Martínez Arbizu P.	Three new species of <i>Cerviniella</i> Smirnov, 1946 (Copepoda: Harpacticoida) from the Arctic
121	Kitahashi T. and Shimanaga M.	Spatial changes in community structure of harpacticoids around trenches
107	Kudryavtsev A., Pawlowski J. and Hausmann K.	Amoebozoa in deep-sea samples from the western Atlantic revealed by the DIVA3 expedition on board RV METEOR
61	Levin L.A., Rouse G., Warén A., Goffredi S., Orphan V., Rathburn A., Grupe B., Cook G., Perez E. and Ussler W.	Hydrothermal seeps: the best of both worlds
84	Lisney T.J. and Bozzano A.	Scotopic optical sensitivity in Chondrichthyes
39	Long D. and Baco A.	Distribution of deep-sea corals in the Makapu'u coral bed, Hawaii, and temporal changes in crinoid abundance
51	Longmore C., Neat F., Trueman C., Milton A. and Mariani S.	Dwelling in the deep: population structure and habitat use in the deep-sea macrourid <i>Coryphaenoides rupestris</i>
52	Longmore C., Neat F., Trueman C., Milton A. and Mariani S.	Life history of a long dark fish in a deep dark ocean: <i>Aphanopus carbo</i> in the North Atlantic
9	Lucas Y., Moreira J., Parapar J., Urgorri V. and García-Regueira X.	Deep-sea syllids (Annelida: Polychaeta) from 'DIVA-Artabria I' project (2002 expedition) in the continental shelf and upper slope off Galicia (NW Spain)
10	Lucas Y., San Martín G., Sikorski A. and Moreira J.	A new genus and species of Syllidae (Annelida: Polychaeta) from deep-sea areas off Norway with unusual morphological characters and uncertain systematic position
62	Marteinsson V.T., Hobel C.F.V., Hreggviðsson G.Ó., Reynisson E. and Kristjánsson J.K.	Microbial diversity of the Grímsey high-temperature vent field on the subpolar Mid-Atlantic Ridge
122	Matos F.L., Hilário A., Moura C.J., Ravara A., Rodrigues C.F. and Cunha M.R.	Colonization of artificial substrates in mud volcanoes from the Gulf of Cadiz – macrofauna assemblages

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123	Mechó A., Ramírez E., Aguzzi J., Canals M., Calafat A., Lastras G., Sanchez A., Smith C. and Company J.B.	Video quantitative survey of western mediterranean open slope communities by ROV (Remote Operated Vehicle)
124	Mechó A., Ramírez E., Aguzzi J., Sardà F. and Company J.B.	Taxonomical composition and seasonal differences of megabenthic and benthopelagic invertebrates (non-crustaceans) in Western Mediterranean open slope and canyon
102	Mercier A., Schofield M. and Hamel J.-F.	Evidence of dietary feedback in a facultative association between deep-sea gastropods and sea anemones
40	Mercier A., Sun Z. and Hamel J.-F.	Reproductive biology, including spawning periodicity and development, of the deep-sea scleractinian coral <i>Flabellum angulare</i>
77	Miguez-Rodríguez L.J., Moreira J., Díaz-Agras G., Abad M. and Urgorri V.	Distribution and composition of deep-sea echinoderm assemblages (Holothuroidea, Echinoidea and Ophiuroidea) along a bathymetric transect off Golfo Ártabro (Galicia, NW Iberian Peninsula)
41	Molodtsova T.N. and Budaeva N.E.	Cosmopolitans and widely distributed species of black corals: case study for the North-East Atlantic
11	Moreira J., Parapar J. and Lucas Y.	New data on deep-sea sphaerodorids (Polychaeta, Sphaerodoridae) from Iceland and NW Spain (BIOICE and Diva-Artabria projects)
12	Moreira J., Parapar J., López E., Gambi M.C. and Ramos A.	Epibenthic polychaetes of the Bellingshausen Sea (Antarctica) collected by the Spanish Bentart project
13	Moreira J., Parapar J., Lucas Y. and Urgorri V.	Polychaetes from the continental shelf and upper slope off Golfo Ártabro (NW Spain). Results of the 'Diva-Artabria' 2002 and 2003 expeditions
78	Neal L., Mincks S.L., Smith C.R. and Glover A.G.	Polychaete species diversity on the deep West Antarctic Peninsula shelf
63	Nunes-Jorge A., Duperron S. and Gaudron S.M.	In situ hybridization with HRP end-labelled oligonucleotide 18S rRNA targeting probes for the identification of larvae and juveniles from chemosynthetic ecosystems

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79	Ohkawara N., Gooday A.J., Tsuchiya M. and Kitazato H.	The distribution and species diversity of deep-sea Foraminifera from the equatorial Pacific
125	Packer M., Sherlock E. and Taylor H.	How an internet accessible database is helping us protect historical deep sea samples from the Challenger Expedition of 1872-76
42	Pante E., France S.C., Watling L. and Samadi S.	Biogeography of the pan-distributed deep-sea coral genus <i>Chrysogorgia</i>
103	Papiol V., Fanelli E., Cartes J.E. and Brunet C.H.	Evidence of resource partitioning in deep-sea invertebrates based on stable isotope and pigment analyses
14	Parapar J., Gambi M.C., Rouse G.W. and Moreira J.	On the taxonomy and distribution of the deep-sea species <i>Axiokebuita minuta</i> (Hartman, 1967) (Polychaeta; Scalibregmatidae)
15	Parapar J., Moreira J., Helgason G.V. and Jirkov I.	Taxonomy and distribution of the genus <i>Terebellides</i> and family Opheliidae (Polychaeta) in Icelandic waters, collected by the BIOICE project
89	Pétursdóttir H., Gíslason Á. and Falk-Petersen S.	Fatty acid compositions of muscle, liver and skull oil in deep-sea redfish <i>Sebastes mentella</i> over the Reykjanes Ridge
126	Pusceddu A., Dell'Anno A., Zeppilli D., Corinaldesi C., Gambi C., Mea M., Bezerra T., Vanreusel A., Pape E. and Danovaro R.	Microscale distribution, diversity and functioning of deep-sea benthic community in Atlantic Ocean and Mediterranean Sea
43	Ragnarsson S.A., Burgos J.M. and Ólafsdóttir S.H.	Cold water coral research in Iceland
31	Ramirez-Llodra E.Z., Company J.B., Sardà F. and Coll M.	Litter accumulation at bathyal and abyssal depths in the Mediterranean Sea
127	Rapp H.T. and Schander C.	Macrofauna of shallow and deep hydrothermal vent fields on the mid-ocean ridges north of Iceland

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16	Rapp H.T., Janussen D. and Tendal O. S.	Calcareous sponges from bathyal and abyssal depths of the Weddell Sea -- first record of deep-sea <i>Calcarea</i> in the Antarctic Ocean
96	Raymond E., Johnson S. and Vrijenhoek R.	Presence of <i>Osedax</i> on seal bones in the Monterey submarine canyon
17	Reed A.J., Holland J.S., Linse K. and Thatje S.	A re-description of the deep-sea protobranch bivalve <i>Ledella ultima</i> (E. Smith, 1885) with notes on reproduction and ecology
104	Reid W.D.K., Wigham B.D., Polunin N.V.C., Sweeting C.J. and McGill R.A.	Benthic trophodynamics on the Mid-Atlantic Ridge: a stable isotope approach
24	Ribeiro P., Menezes G., Neat F. and Stefanni S.	Preliminary results on molecular phylogeny for genus <i>Deania</i> (Elasmobranchii: Centrophoridae) from the NE Atlantic with implications on the taxonomy of the group
25	Riehl T.	Morphology and DNA to complement each other in deep-sea isopod taxonomy
97	Romano C., Company J.B. and Martin D.	Wood-boring bivalves from a NW Mediterranean deep sea canyon: abundance and biomass of <i>Xylophaga</i> spp. (Mollusca, Bivalvia)
80	Rothe N., Gooday A.J., Cedhagen T. and Hughes J.A.	Biodiversity and distribution of the genus <i>Gromia</i> (Protista, Rhizaria) in the deep Weddell Sea (Southern Ocean)
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Abstracts of Oral Presentations

Behavioural rhythms in deep-water continental margins and the deep-sea

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Unità di Ricerca per l'Ingegneria Agraria (Agricultural Engineering Research Unit)

The presence of behavioural rhythms has been usually studied in organisms of coastal areas in relation to day-night and tidal cycles, but their presence in demersal fauna inhabiting light-limited or aphotic deep-sea regions remain poorly characterized. Here, we present evidences on the photic and also hydrodynamic regulation of activity rhythms in deep-sea species of the western Mediterranean and the Japanese Sea. In the Mediterranean, day-night hauling was carried out in different depths (i.e. 900, 1050, 1200, 1350 and finally, 1500 m) during different seasons of 2009 (i.e. March, May, September, and October). Collected fish and decapod species were sorted and their numbers standardized to km². Marked catch variations were obtained above and below the twilight zone border, as proxy of population behavioural rhythms. In the Japanese Sea (i.e. Sagami cold-seep; 1100 m depth), a continuous 62-days length video from JAMSTEC platform (i.e. from 17-04 to 18-06 of 1999) was automatically processed with a newly elaborated software for image recognition. Three target species were analyzed: eelpouts (Zoarcid fishes), red crabs (*Paralomis multispina*), and snails (*Buccinum soyomaruae*). Time series of visual counts were obtained and analysed using chronobiological statistic tools. That analysis was combined with contemporary physical measurements collected at the AJMSTEC platform, which revealed the presence of internal tide fluctuations. Marked spring/neap modulation of rhythms was found only in eelpouts. Outcomes of both studies are discussed focusing on the ecological importance of photic and aphotic cues in the regulation of deep water and deep-sea species biorhythms when these are swimmers, walkers or crawlers.

Ecosystem functioning in the deep sea: the trophic biology of the holothurian *Molpadia musculus* at 3,500 m in the Nazaré Canyon, Portuguese Margin

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Megafaunal organisms can play a key role in the deep-sea ecosystem functioning. At 3,500 m depth in the Nazaré Canyon, unexpected high abundances of the infaunal holothurian *Molpadia musculus* were found, but reasons for such a rise is still uncertain. Two main hypotheses were investigated: a) the existence of trophic interactions with prokaryotes to enhance its ability to digest sediment and b) the bioavailability of potential food sources. To address these questions, sediment samples and holothurians were collected by ROV Isis and experiments were conducted in situ by using incubations in chambers to collect faeces from the holothurians. Prokaryotic abundance, diversity and community were studied by using two

fingerprinting techniques (T-RFLP and ARISA) and by epifluorescence microscopy coupled with CARD-FISH. Bioavailability of food sources was checked by biochemical composition of the sediment. The results demonstrated that *M. musculus* gut hosts a significant abundance of both Bacteria and Archaea and possesses specific assemblages between the holothurian gut, the surrounding sediments and faeces. This suggests the presence of a highly specific microenvironment able to support a specialised gut bacterial flora, which may help *M. musculus* in assimilating or digesting sedimentary OM. Our results also indicate that prokaryotes most probably do not contribute as a significant food source for their metabolism. *Molpadia musculus* appears to be using proteins as the main compound, being degraded through the gut. Lipids are also used but to a lesser extent and carbohydrates are not broken down or utilized at the time of sampling. We estimated that these holothurians can remove about 0.5 g of biopolymeric C and 0.06 g N m⁻² d⁻¹ and therefore might have a crucial role in benthic trophic-dynamics, OM early diagenesis and in the cycling of organic C and N in the deep-sea floor of the largest submarine canyon of the European margins.

A comparison of the fauna of cobalt-rich and non cobalt-rich seamounts

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Seamounts of the central and western Pacific face increasing threat from proposed cobalt-rich manganese crust mining. Very little data on the fauna of cobalt-rich crusts are available to inform future environmental management initiatives. Although an unlikely target for mining, the Hawaiian Archipelago falls on the periphery of the cobalt-rich area. Using the Hawaii Undersea Research Laboratory's submersible and ROV video log database, we converted 30,000 records to a species by dive matrix. Multivariate analyses were conducted to compare the fauna of cobalt-rich to non-cobalt rich crusts, to determine factors that might drive faunal composition patterns, as well as to examine general faunal distributional patterns on seamounts. There was no difference in community structure between cobalt vs non cobalt-rich sites. There also did not appear to be differences in community structure that are related to the geomorphological classification (seamount, island, bank, or atoll) of the features. Instead, sites were strongly structured by depth with location as a secondary factor.

Long-term change in structure of the deep-water fish community of the Porcupine Seabight and Abyssal Plain

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A severe scarcity of life history and population data for deep-water fish is a major impediment to successful fisheries management. Long-term data for non-target species and those living deeper than the fishing grounds are particularly rare. We analyzed a unique dataset of scientific trawls made from 1977–89 and 1997–2002, at depths from 800 to 4800

m. Over this time, overall fish abundance fell significantly at all depths from 800 to 2500 m, considerably deeper than the maximum depth of commercial fishing (c. 1600 m). Analysis of community structure using multivariate methods reveals how the relative abundances of the various fish species have also been altered, with some of the greatest changes being observed at and beyond the margin of the fishery (c. 2000 m). The impacts of fishing spread well beyond the actual areas fished, and impact target and non-target species equally.

Deep-sea fishes and coral habitat associations on the Grand Banks, Newfoundland

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Small-scale associations of deep-sea corals and fishes are difficult to infer from trawl surveys that are the basis for much of what is known. To assess this linkage at a biologically meaningful scale, we analyzed video of deep water (200 – 2200 m) habitats collected on the slope of the Grand Banks south of Newfoundland in 2007 using the remotely operated vehicle ROPOS. Video frames were scored for depth, bottom type, coral species and size, evidence of coral damage and trawl marks, and fish species, size, and behaviour. We found over 19,000 fishes representing more than 70 species, and 26 coral species forming over 160,000 colonies. Coral habitats included large *Keratoisis ornata* thickets, sea pen meadows over 1 km in length, and expansive fields of *Acanella arbuscula*. Redfish (*Sebastes* sp.) and *Synphobranchus kaupii* were by far the most numerous fishes, followed by macrourids, particularly *Coryphaenoides rupestris*. *S. kaupii* was ubiquitous in upper and middle slope habitats, whereas preliminary analyses show that redfish and longfin hake (*Phycis chesteri*) were found in coral and other highly structured habitats. Two species at-risk in Canadian waters, spotted wolffish (*Anarhichas minor*), and northern wolffish (*A. denticulatus*) were observed in dense coral habitats. Other findings include observations of orange roughy (*Hoplostethus atlanticus*) in *K. ornata* thickets, false boarfish (*Neocyttus helgae*) on a bedrock ledge, and deepsea cat shark (*Apristurus profundorum*) in fine substrate habitat. These associations have important implications for habitat conservation and fishing impacts.

Effects of ocean acidification on metabolism and acid-base balance in brachiopods (*Laqueus californianus*): implications for the fossil record and the future

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MBARI
SIO

Lamp shells (brachiopods) were a dominant and diverse element of the benthos in Paleozoic seas, but crashed during the end-Permian extinction from thousands of species to only a few hundred. Ocean acidification and hypoxia caused by massive volcanism are among the hypotheses to explain the dramatic loss of diversity, but have not been tested experimentally. We examined the effects of exposure to acidified ocean waters (corresponding to atmospheric CO₂ levels of ~380 – 1000 ppm) on adult brachiopods (*Laqueus californianus*) collected from the continental shelf off central California. Exposure to pH of 7.2 to 7.6 units led to metabolic depression, collapse of the external to internal pH and pCO₂ gradient, and reduced survival. Loss of acid base balance will also impair respiration rates, due to the reduced binding affinity of brachiopod hemerythrin under lower pH. The combined consequences of the metabolic

impacts of ocean acidification are likely to result in reduced individual growth, survival, and reproduction, leading to reduced population growth rates and resilience, and greater likelihood of extinction. These results support the hypothesis that ocean acidification contributed to episodes of brachiopod extinction documented in the fossil record and suggest that future ocean acidification may also be stressful for *Laqueus* sp. and other brachiopod species.

Reproductive biology of the cold-water coral *Acanella arbuscula*, Northwest Atlantic

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Over the past few decades there has been substantial research on the reproductive biology of shallow-water anthozoans. Egg size, mode of reproduction, fecundity, and gametogenic cycles are well documented in this group. Much less is known on the reproductive characteristics of anthozoans found below the photic zone. Recent effort has been made to characterize the reproductive processes of deep-water scleractinians, however the reproductive biology of octocorals, especially members of the Order Alcyonacea, remains poorly documented. Reproductive characteristics of the cold-water branching coral *Acanella arbuscula* (Order Alcyonacea (ITIS)) of the Northwest Atlantic have been examined. Colonies were collected from the Gully Marine Protected Area (MPA) on the Scotian shelf in July 2007 using the ROV ROPOS between depths of 1750 and 1800 meters, and from the eastern slope of the Flemish Cap during May and July of 2009 between depths of 700 and 1130 meters using both a rock dredge and box corer. Using standard histological techniques, colony sex, intra-colony variation in the number and size of the sexual products, mode of sexual reproduction, and some aspects of gametogenesis were examined. Initial examination of eight colonies of *A. arbuscula* revealed that this species is gonochoristic. Oocyte size, and both the number and size of the sperm cysts differs depending on polyp position on a branch, with oocyte diameter being significantly higher in distal polyps, and the total number of sperm cysts and their diameters being significantly lower in proximal polyps. Deep-water corals are being removed and damaged by anthropogenic activities at an unprecedented rate, an action in which the consequences are not fully understood. Information on their reproduction may provide insight into how these species re-establish in an area after disturbance, and may be useful for their conservation.

A quantitative assessment of anthropogenic activities in the deep North East Atlantic

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Human activities on the deep-sea floor are of increasing concern. While activities within Exclusive Economic Zones have been the focus of previous assessments, no study has quantified the extent of activities or determined the relative severity of individual impacts for the deep sea. The OSPAR maritime area of the North East Atlantic was examined because it

is one of the areas most heavily impacted by human activities and it was assumed data would be available and comprehensive. While data for some activities were readily available, data for other activities were difficult to obtain. Despite the limitations of the data, the information available has been used to map and estimate the spatial extent of five major human activities in the North East Atlantic that impact the deep-sea floor: submarine cables, marine scientific research, oil and gas industry, historical dumping of radioactive waste and munitions and chemical weapons and commercial bottom trawling. The extent of each activity has been quantified for a single year, 2005. Bottom trawl fisheries were found to affect an area of seafloor orders of magnitude greater than all the other the activities investigated. While this is not necessarily a surprise the study provides the first quantitative estimate of impacts and their relative severity. While initiatives to improve integration and dissemination of scientific data are underway, data relating to other activities frequently remain inaccessible, incomplete and fragmented. To ensure environmentally sustainable management of the deep ocean in the future, significant improvements are required in reporting requirements, data standards and access as well as more systematic analysis of these data

Longer-term dynamics of megafaunal assemblages from the Arctic observatory HAUSGARTEN (eastern Fram Strait, 79°N)

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In 1999, the Alfred Wegener Institute for Polar and Marine Research established the first deep-sea observatory beyond the polar circle, HAUSGARTEN, to study the long-term dynamics of bathyal benthic communities. It comprises a bathymetric transect (1000–5500 m) of nine stations, an experimental arena in the centre (2500 m) and six stations along a latitudinal transect (2500 m). These stations have been sampled annually to determine variations in biological, geochemical and sedimentological parameters over time. Megafaunal assemblages from the central HAUSGARTEN station were investigated by a towed Ocean Floor Observation System in 2002, 2004, 2007 and 2008. Agassiz trawls provided physical samples for ground-truthing. The manual analysis of 30 images per year indicates a significant decrease in total megafaunal densities between 2002 and 2004 followed by an increase in 2007 and 2008. The same trend was found for sea lilies (*Bathycrinus carpenterii*), soft corals (*Gersemia fruticosa*) and gastropods (*Mohnia* spp.). The numbers of deposit-feeding sea cucumbers (*Elpidia heckeri*), however, grew between 2002 and 2004 and fell afterwards. Our results from manual image analysis will be compared with those obtained from automated image analysis and discussed in the context of changes in environmental parameters measures at the same time at HAUSGARTEN central.

Temporal variation in abundance, recruitment and distribution of a commercially exploited deepwater fish, the roundnose grenadier *Coryphaenoides rupestris*

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The roundnose grenadier *Coryphaenoides rupestris* is a long-lived deepwater fish which reaches ages of 70 years or more and attains maturity at the age of 8–12 year. Its life history strategy and limited area of distribution in the deep Skagerrak basin (300–720 m) may make

the grenadier in this area particularly vulnerable to overexploitation, but also a good candidate for studies of population-level impacts of fisheries. The 2003–2005 major expansion of the targeted grenadier fishery followed by a complete closure created an exceptional opportunity to study such impacts on a deepwater fish population. Data from annual Norwegian *Pandalus borealis* surveys conducted since 1984 were used to analyse abundance variation, recruitment patterns, variation in size structure, and spatial distribution. This fisheries-independent data series is perhaps the only one of its kind providing information for a quarter of a century on what appears to be a self-contained commercially exploited population of a macrourid fish population. Recruitment appeared intermittent with only a couple of elevated pulses through the time series, and in particular a single strong yearclass that supported the expansion in the fishery in 2003–2004. Post-fishery abundance was low compared with the 1990s and early 2000s, but comparable with the 1980s.

Metagenetic analysis of biodiversity patterns in deep-sea benthic meiofaunal communities

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Deep ocean sediments harbor vast numbers of eukaryotic meiofauna, yet there is a well-recognized gap in the taxonomic understanding of their biodiversity. The present study represents the first comprehensive molecular assessment of deep-sea metazoan communities using new, high-throughput 454 sequencing methods. Two diagnostic regions of the 18S rRNA gene were amplified from environmental DNA samples representing a total of 10 sites (5 bathyal/abyssal Pacific sites, 5 abyssal Atlantic sites and 2 shallow water sites). Purified PCR products were sequenced on a GS FLX Titanium platform, returning a total of 1.2 million sequence reads ranging from 350–450 bps in length. The recently developed OCTUPUS pipeline was used to process raw data, performs quality checks on all sequences, and subsequently group sequences into Operational Clustered Taxonomic Units (OCTUs) using different pairwise sequence identity cutoffs (95–99%). All analyses recovered a diversity of eukaryotic taxa, with similar taxonomic compositions recovered from independent analyses of the two rRNA regions. Broad taxonomic compositions were roughly consistent with expectations for benthic meiofaunal communities. These preliminary data suggest some very interesting observations regarding OCTU distribution and membership. Based on a 95% clustering (a value that clusters multiple, closely related species based on control experiments), there are many cases where the same OCTU is found in multiple localities from both Pacific and Atlantic deep-sea locations. At a 99% cut-off value, many of these shared OCTUs were split up into separate OCTUs according to geography, suggesting that a 95% cut-off lumps many species that represent geographically restricted (but closely related) taxa. However, even at a 99% clustering there remained a number of nematode OCTUs (and many other meiofaunal taxa) which appear to be abundant in both Pacific and Atlantic habitats. Further analysis is being conducted to fully investigate these patterns, but preliminary glimpses from 454 data suggests that benthic meiofaunal communities in the deep-sea are comprised of a mixture of cosmopolitan species and species that are restricted to single localities.

Benthic responses to natural iron fertilisation in the oceans

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Natural ocean iron fertilization, stimulated by iron leached from oceanic islands, occurs within the High Nutrient Low Chlorophyll (HNLC) expanse of the Southern Ocean. Studies of these areas allow the comparison of closely-situated abyssal benthic communities exposed to different surface water productivity regimes. This paper compares two localities around the Crozet Islands in the southern Indian Ocean. The sites are 460 km apart, both at a water depth of about 4200 m. No physical barriers separate the sites, and they lie in the same water mass. East of the Crozet Plateau there is a seasonal phytoplankton bloom stimulated by elevated iron concentrations in surface waters (+Fe site). This site had a carbon flux at 3000 m water depth 2.5 times greater than at the second site situated in HNLC waters south of the islands (-Fe site). There is a marked contrast in the biomass of the megabenthos at the two sites mirroring the measured organic carbon flux. In addition, there were major differences in megafaunal community structure at the two sites. We attribute the differences to the characteristics of organic matter supply (quantity, timing and quality). The most abundant species encountered, the holothurian *Peniagone crozeti* Rogacheva and Cross 2009, has been reported only around the Crozet Islands and almost exclusively at the +Fe site. How can such an abundant organism apparently have such a restricted geographic distribution? Other faunal differences between the two sites, and the remarkable similarity of the +Fe site with eutrophic abyssal regions of the NE Atlantic emphasise the importance of surface water productivity on benthic community structure. In addition, it is clear that long-term large-scale geo-engineering via extensive manipulation of primary production would have significant effects on deep-sea communities.

Distribution of epi- and mesopelagic scattering layers around Indian Ocean seamounts

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Seamounts often harbour considerable aggregations of fish and micronekton, some of which are targeted by fisheries. These aggregations are thought to be sustained by localized trophic subsidies, provided by mechanisms like the topographic blockage of descending zooplankton and lateral advection of allochthonous material. During an explorative study of the largely unknown pelagic ecosystem of the Southwest Indian Ocean Ridge in 2009 we investigated the vertical and geographical distributions of epi- and mesopelagic scattering layers around six seamounts and at two off-ridge sites. Scattering layers were observed in the entire study area and at all depths to approx. 1500 m using 18 and 38 kHz vessel-mounted split-beam echosounders. Additional observations of epipelagic scattering layers down to approx. 150 m

were made using 120 and 200 kHz transducers. The dominant feature throughout the survey region was an approximately 300 m thick mesopelagic scattering layer with a daytime depth between 300 and 800 m. This layer was notably influenced by four of the surveyed seamounts, both directly by physical interference and increased downstream turbulence as well as indirectly through seamount-associated aggregations of fish and micronekton. Overall backscatter was substantially higher around shallow and intermediate seamount summits compared to adjacent waters, which can be attributed to large pelagic schools. This was not the case for two deep seamounts and the off-ridge sites. The spatial variation in backscatter of different vertical layers is described in relation to topography and local flow patterns as well as important large scale oceanographic features, notably the Southern Subtropical Front. Further acoustic sampling during 24h-long CTD deployments provided insights into the diel dynamics of the scattering layers on seamount summits including the interception of downward moving scatterers by midwater aggregations at dawn.

A comparison of neighbouring deep-sea basins. High genetic distances in species of the genus *Chelator* Hessler, 1970 (Isopoda: Desmosomatidae)?

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During DIVA-2, isopods were sampled with RV “Meteor” at eight deep-sea stations in the Cape Basin, the Angola Basin and the Guinea Basin. The analyses on DIVA-2 isopods drew a complex picture of genetic distances within the genus *Chelator* Hessler, 1970 (Desmosomatidae Sars, 1897). 16S rDNA sequences could be retrieved from twelve specimens. Morphologically, these belonged to two species. One of these was collected in both, the Guinea and Cape Basins. The second species was collected only in the Guinea Basin. Within the Guinea Basin several specimens with similar morphology (“*Chelator* sp. 1”) show extremely high divergence (14.5% p distance) between two distinct haplotype networks. Within each network distances have a value of 0% and 6.5%, respectively. The Haplotype network in the Cape Basin is conserved, presenting 0.1% p-distance. Between “*Chelator* sp. 1” haplotypes of the different the basins, a p-distance of 12.5% was found. Between congeneric species “*Chelator* sp. 1” and “*Chelator* sp. 2” a p-distance of ~32% was measured, regardless of the origin of the specimens. On the one hand, these results indicate the presence of at least three "groups" in “*Chelator* sp. 1”. The morphology of these specimens is presently re-evaluated.

Respiratory response of the deep-sea lysianassoid amphipod *Stephonyx biscayensis* (Chevreux, 1908) to temperature and hydrostatic pressure

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Widespread depth zonation of fauna on continental margins is well documented. Whilst increasing hydrostatic pressure with depth has long been considered a factor contributing significantly to this pattern, discussion of the relative significance of decreasing temperature with depth has continued. High pressure and low temperature are known to affect enzymatic proteins and lipoprotein membranes similarly, suggesting that combined hydrostatic pressure and temperature effects may cause observed limits to species’ depth ranges. This study

investigates the physiological tolerances of the deep-sea lysianassoid amphipod *Stephonyx biscayensis* to temperature (1, 3, 5.5, 10°C) and pressure (1, 50, 100, 150, 200, 250, 300 atm) by measuring the rate of oxygen consumption. This species is common at depths between 500 and 2000 metres across the North-East Atlantic Ocean from Iceland to the Cape Verde Islands, but has also been reported at similar depths in the Gulf of Mexico and the Caribbean Sea. The effect of pressure on respiration rate is revealed to be dependent on temperature, with physiological impairment observed at pressure greater than the species natural bathymetric distribution at 1 and 3°C, and restricted to pressure equivalent to greater than 2500 metres depth at 5.5°C. In stark contrast at 10°C no physiological impairment is apparent at pressures equivalent to 3000 metres depth. These results implicate the combined effect of pressure and temperature in contributing to the phenomenon of a biodiversity bottleneck between 2000 and 3000 metres. This suggests that there is potential for bathymetric range shifts in response to global climate change, with coincident potential for shifts in ecosystem dynamics.

Depth zonation of deep-sea benthos on the margin of the Norwegian Sea – Results from MAREANO

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The project MAREANO is mapping marine benthic habitats and biodiversity in Norwegian waters. The mapped areas cover depth from 40 to 2700 m with troughs, ridges, canyons, mega sand waves, cold seeps and coral reef areas. A wide set of sampling techniques is applied to get a representative picture of the diversity of bottom fauna. The continental slope off Northern Norway represents a strong gradient in hydrography. Above ~600 meters, temperature stays above +0.5°C, at 600–900 meters there is a transition layer with between 0.5 and -0.5°C, below the temperature is between -0.5 and -1.1°C. Video observations show a corresponding gradient in dominating megafauna and these results will be presented here. At 200–500 m depth areas with sponge communities and the basket stars (*Gorgonocephalus eucnemis*) are common. In deeper water (700–900 m) the gorgonian coral *Radicipes* sp. was observed. On the soft bottom on the lower slope (900–1100 m) small crustaceans (Peracarida) were found living on stalks and tube of other organisms. The sea pen *Umbellula encrinus* seems to be restricted to this depth zone in canyons. The megafauna in the deepest areas (2200–2700m) appear to be common for the deep northern parts of the Atlantic and the Norwegian Sea. This arctic fauna was dominated by the holothurians *Elpidia glacialis* and *Kolga hyalina*, the stalked crinoid *Rhizocrinus lofotensis* together with the crustaceans *Bythocaris leucopis* and *Saduria* sp. and the sea urchin *Pourtalesia* cf. *jeffreysi*. The fauna is not species rich, but specific for the arctic deep-water. The richness and abundance of fauna at these depths was very low and it is clearly higher on the shallower slope. However, there is a clear trend that habitat forming organisms have an increasing role as local biodiversity hotspots with increased depth.

Fungal communities in deep-sea hydrothermal ecosystems

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Boundaries for fungal life in deep marine ecosystems have been recently extended. Several papers reported the presence of fungi in deep-sea hydrothermal vents (Edgcomb et al. 2002; Lopez-Garcia et al, 2003; Gadanho & Sampaio, 2005; Lopez-Garcia et al. 2007), anoxic deep-sea waters (Takishita et al. 2005; Zuendorf et al. 2006, Stoeck et al. 2006; Edgcomb et al. 2009) and subsurface deep-sea sediments (Raghukumar et al. 2004; Damare et al. 2006; Damare & Raghukumar, 2007). These papers revealed the presence of fungi and some nucleotidic sequences were novel. However, the occurrence of fungal communities (filamentous fungi and yeasts) at deep-sea hydrothermal vents remains an underexplored topic. Consequently, our group initiated a research program that focused on isolation of fungi from samples collected at deep-sea hydrothermal vents of Mid-Atlantic Ridge and East Pacific Rise. Whole results allowed (i) to describe taxonomic diversity of deep-sea filamentous fungi and yeasts; (ii) their physiological characteristics under different conditions of temperature, salinity and hydrostatic pressure which suggest isolation of endemic and ubiquitous species; (iii) to reveal distribution heterogeneities between and inside hydrothermal sites and frequent fungal association with endemic dominant animal species; (iv) to compare amplified rDNAs from fungal isolates with those directly amplified from hydrothermal samples; (v) to assess the presence of yeasts inside animal communities with in situ hybridizations and (vi) to describe a new species in the *Candida* genus, submitted as *Candida marinus*. Our results describe for the first time the presence of filamentous fungi at deep-sea hydrothermal vents and enlarge our view of the microbial diversity in these extreme ecosystems using both culture-dependent and culture-independent methods (Burgaud et al, 2009; Le Calvez et al. 2009). It finally suggests future works to study fungal communities in oceanic environments.

New insights on the diversity among microbial communities associated to the hydrothermal shrimp *Rimicaris exoculata*: a double symbiosis

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Rimicaris exoculata dominates the megafauna of some Mid Atlantic ridge hydrothermal vent sites. This species harbors a rich community of bacterial epibionts inside its gill chamber. Previous data indicated that a single phylotype affiliated to Epsilonproteobacteria was dominant and assumed to be a sulfide-oxidizing bacteria. However, attempts to cultivate them were unsuccessful. Moreover, *Rimicaris exoculata* gut has been shown to harbour microbial communities, affiliated to tree phyla: Epsilonproteobacteria, Mollicutes and Deferribacterales. Most of these lineages have not been retrieved in the outer environment which suggest a local digestive microflora. In order to describe these two microbial communities several approaches have been used, comprising microscopy (SEM, TEM, FISH), molecular biology (16S

diversity, specific functional genes), as well as in vivo experiments at in situ pressure in the presence of various electron donors. Our microscopic observations, as molecular data indicated a wider diversity (both in morphology and phylogeny) than previously described for the gill chamber epibiotic community, with Epsilonproteobacteria lineages but also Gammaproteobacteria. We observed bacterial intracellular sulfur- and iron-enriched granules and some methanotrophic-like bacteria cells for the first time. Genes, characteristic of methane-oxidizing (*pmoA*) and sulfide-oxidizing (APS) bacteria, were also identified. These results suggested that three metabolic types (iron, sulfide and methane oxidation) may co-occur within this community. As this shrimp colonizes chemically contrasted environments, the relative abundance of each metabolic type could vary. This will be discussed. Regarding the gut microbial community, we analysed shrimps gut dissected after recovery, or long term starvation experiments at in situ pressure. Our results indicated a wider diversity than previously assumed and, for the first time, microscopic analyses (SEM, TEM and FISH) indicated the presence of long microbial filaments in contact with gut epithelial cells, between microvillousities. The role of this permanent digestive microflora will be discussed as well as their possible acquisition.

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Feeding of stomiiform fishes of the northern Mid-Atlantic Ridge

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Few previous studies have focused specifically on the role of the mid-ocean ridges in the ecology of pelagic fishes. This study centers on a dominant nekton component of the mid-Atlantic mesopelagic ichthyofauna - the Stomiiformes - and their food resources including zooplankton and other nekton. Its main goal is to characterize the diets of several species of these midwater fishes towards understanding the trophic pathways of the deep-pelagic nekton of the northern MAR. The study material was provided by the 2004 G. O. Sars Expedition as part of the international Census of Marine Life field project MAR-ECO (www.mar-eco.no). Twelve species of Stomiiformes were dissected and diet items were identified to the lowest taxonomical level possible. The main prey groups found in guts were amphipods, copepods, ostracods, euphausiids, fishes, chaetognaths, decapods, pteropods, cephalopods and jellyfish, with different occurrences and proportions depending on the predator species, represented 3 main feeding strategies: (zoo)planktivory, piscivory and in some cases omnivory, further explored in this talk. Numbers of prey were converted in biomass using wet weight measurements or instead length-weight regressions from literature, in cases when the prey was too digested. Feeding guilds for the predator species were determined. Future work includes calculation of daily ration and predation impact of the midwater fish assemblage on their prey in an attempt to design a food web model of the nekton community associated with the MAR.

A report at year 6 for long-term colonization of artificial sulfidic substrate by chemosynthetic fauna

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The discovery of chemosynthetic tubeworms on the decomposing agricultural cargo of a deep shipwreck reported by Dando raised the possibility that these organisms could be attracted to manmade artificial substrates. If substrates could be devised with the necessary output of hydrogen sulfide, questions such as larval dispersion, community succession, and organism growth rates could all be addressed experimentally rather than be dependent upon exploration and discovery. Two initial prototype biogenerators were deployed at a seep site in the Gulf of Mexico in 1995 and visually monitored during subsequent submersible operations. Settlement and growth of *Lamellibrachia* sp. was observed after 5 years. On recovery a total of 506 small specimens were found. Extensive device deployment began in 2003. Seventy two devices were deployed by submersible on the upper slope of the Gulf of Mexico following an ANOVA design to examine the effect of proximity to seeps and device size. Ninety six devices were surface deployed in 6 clusters of 16 in water deeper than 2500 m along the US Atlantic and Gulf of Mexico coast. A portion of the upper-slope deployments were harvested after 3 years in 2006. Probe profiles indicated high levels of sulfide generation. Colonization by *Lamellibrachia* was low and limited to close proximity to seeps. Devices had, in addition, been colonized by lucinid clams at greater distances from seeps. Due to the low settlement, 18 devices were left on bottom for additional monitoring. In 2009 visual and image inspection showed more extensive colonization and growth by tubeworms. The devices were left on bottom for additional monitoring. Relocation and examination of the deeper widespread deployments remains to be undertaken. Use of artificial substrates in seep research has proven successful but requires a time commitment of 5 to 10 years.

Fishing deep: longline surveys in mid-Atlantic seamounts

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Deep-sea living resources have gained importance over the last decades in commercial fisheries as a result of over-exploitation of the coastal stocks. In order to achieve a suitable management strategy for these fisheries, it is essential to understand the demographic and life-history characteristics of the poorly studied deep-sea species. The two cruises, organized within the DEECON project (“Unravelling population connectivity for sustainable fisheries in the Deep Sea”), aimed to deep-sea fishery on eight Atlantic seamounts located South (Great Meteor, Irving, Plato and Atlantis) and West (Cavala, Voador, Monte Alto and Gigante) of the Central Group of the Azores Archipelago. Fishing was done using two longline gears adapted to the collection of black scabbardfish, deep-sea sharks and shallower demersal species. The fifteen longline sets were deployed along a bathymetric gradient between 150 and 2000 m. During the surveys data on fishing effort, catches by species beside other biological and oceanographic information were collected. For the first cruise a total of 34 teleosts and 19 elasmobranches species were collected. In the second cruise a total of 25 teleosts, 16 elasmobranches and 3 crustaceans species were caught. For both cruises the teleosts fishes dominated the catches in number and *Helicolenus dactylopterus dactylopterus*

was the predominant species. However with the depth increment the elasmobranches catches became more relevant. Several invertebrates were caught as bycatch, mostly cold water corals and sponges. Most of them were identified and preserved for future studies.

Pelagic food web connectivity in the Central North Pacific Ocean with a focus on deep ocean mid-trophic level groups

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The deep waters of the open ocean comprise the largest habitat on the planet. Yet, little is known about the ecology of the animals that live in the deep sea even though many support production for numerous commercially harvested species. Recent analysis of fishery data from the central North Pacific reports a concurrent shift in relative abundances of increasing mid-trophic level fishes (e.g., *Taractichthys steindachneri*, *Lepidocybium flavobrunneum*, *Gempylus serpens*) and decreasing apex predators (e.g. *Thunnus obesus*, *Prionace glauca*, *T. alalunga*) over the past decade (Polovina et al. 2009). Very little is known about the basic biology and trophic ecology of these increasingly abundant mid-trophic level fishes, many of which primarily inhabit mesopelagic waters. This study provides some of the first food habit data on these large mesopelagic fishes (*Alepisaurus ferox*, *Lampris guttatus*, *Gempylus serpens*), and on the trophic connectivity of their micronektonic prey (small fishes, crustaceans and cephalopods ~2–20 cm). In contrast with previous studies of higher trophic level pelagic fishes (e.g. tunas and billfishes) preliminary diet results indicate greater occurrences of deeper-water prey organisms (e.g. *Sternoptyx* sp., *Phronima* sp., *Platyscelus* sp., *Onykia* sp. A), with differing intra-specific importance of fishes, crustaceans and cephalopods. Stable isotope results show modest separation between key functional micronekton groups (e.g. myctophids, cephalopods, gelatinous organisms, crustaceans), suggesting that these isotopic differences may be evident in as differences in diet in higher trophic levels animals (e.g., predatory pelagic fish). These results are the beginning of a project to examine a diversity of pelagic animals to delineate trophic linkages and understand pelagic energy flow across large vertical depth gradients. Future incorporation of this data into ecosystem-based fishery models (e.g., EwE, SEAPODYM) will provide important model validation, as well as improve model resolution at mid-trophic levels.

The impacts of human activities on seamounts: low resilience of faunal communities to trawling and mining

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Seamounts are the target of major trawl fisheries and are of increasing interest for their mineral resources. Conservation of seamounts is gaining momentum, motivated by the apparently unique ecological status and vulnerability of seamount biota. Here we present

results of recent studies on the vulnerability and resilience of seamount communities to fishing and mining.

Since the 1960s, seamounts have been subject to large-scale bottom trawl fisheries, mainly targeting pelagic armourhead, alfonsino, roundnose grenadier, and orange roughy. Most fish stocks have shown strong declines, and few have proven sustainable. Moreover, bottom trawling commonly causes severe damage to the benthos, with deep-sea corals and associated invertebrate communities being most susceptible. Whilst few taxa are physically resistant to trawling impacts, some can survive in natural refuges inaccessible to trawls. However, most megabenthos is removed, causing the loss of biogenic habitat from large areas of individual seamounts. The resilience of seamounts ecosystems is very low and we have found no evidence that benthic assemblages recover in the short term (10 years) following spatial fishing closures.

The physical impacts of mining could be equally damaging. Polymetallic sulphides occur in areas of hydrothermal venting, where faunal assemblages can have high levels of endemism and are therefore likely to be of high conservation significance. In contrast, we have found the benthos of cobalt-rich ferromanganese crusts on seamounts could be similar to the fauna on non cobalt-rich crusts. Hence, whilst the benthos there remains highly vulnerable to physical disturbance, the long-term effects are hypothesized to be less severe.

Seamount communities generally have low tolerance to human disturbance. Whether seamounts are exploited for their fisheries or their mineral resources, networks of spatial closures, allocated using systematic conservation planning, can be an effective option allowing exploitation and conservation to coexist.

Trophic structure of colonization modules at chemosynthetic environments: a comparative approach

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Vent and cold seep ecosystems sustain cognate faunal communities of high biomasses based on chemoautotrophic production. Many of the invertebrates of these communities are taxonomically allied but only infrequently they share affinities at the species level. What are the colonisation processes both for cold seeps and hydrothermal vents? Under the CHEMECO project, different substrates (Carbonates; Wood Douglas Fir and Grass Dried Alfafa) were used for colonization experiments in both types of environments. The main goal was to understand the initial steps of the colonization and to gain insight on the metabolic pathways at play. We tried to establish the trophic structure of the colonizing modules through stable isotope and fatty acid approach using samples collected from the experiments deployed in the MoMAR hydrothermal sites (Lucky Strike and Rainbow) of the Mid-Atlantic Ridge and in the mud volcanoes of the Gulf of Cadiz (Marcator, Meknes and Darwin). Preliminary results show that the substrates present bacterial fatty acids largely attributed to sulfate-reducing bacteria and sulfide-oxidizing bacteria (Li et al, 2007). Some of these fatty acids are connected to specific sites. Stable isotope results from the colonizing invertebrates will be also discussed in the light of this.

Sensory constraints in temporal segregation in two species of anglerfish (*Lophius budegassa* and *L. piscatorius*)

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Temporal segregation of two ecologically equivalent and sympatric Lophiid species, *Lophius budegassa* and *Lophius piscatorius* (black and white anglerfish) was studied in relation to day-night behaviour and corroborated with morphological variation in sensory organs. These benthic species co-occur in the Mediterranean Sea from coastal waters down to 800 metres. However, *L. piscatorius* extends its bathymetrical range as far as 2600 metres depth. A four-day temporally scheduled trawl sampling was carried out on the Western Mediterranean. Fluctuations in the amount of hauled individuals were used as proxy of behavioural rhythms. Marked temporal catch patterns were found for both species, being *L. budegassa* more abundant at night than *L. piscatorius* which mostly occurred in daytime catches. Observed differences in timing of maximum activity (i.e. catches) were consistent with comparable differences in eye/lens sizes and otolith weight. *L. budegassa*, presented significant heavier otoliths than *L. piscatorius*, in order to increase sound perception, a mechanism that compensates the reduced information that the visual system can perceive at low light intensity. *L. budegassa* showed also larger eye and lens than *L. piscatorius* but only in individuals smaller than 50 cm. In fact, a shift among their trends was observed during growth, as individuals of *L. piscatorius* larger than 50 cm showed larger eyes than individuals of *L. budegassa*, an adaptation to improve optical properties while this species increased its bathymetric distribution in depth. Data are discussed considering that interspecific competition of sympatric and ecologically equivalent species may result in different adaptations to diurnal/nocturnal behaviour sustained by morphological specializations in sensory organs.

Deep-pelagic (0–3000 m) fish assemblage structure over the Mid-Atlantic Ridge relative to the North-Atlantic subpolar front

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Only a tiny fraction of the world's largest volume of living space, the ocean's mid-water region, has ever been sampled. It is one of the least understood areas on earth, so as part of the International Census of Marine Life field project, MAR-ECO, a discrete-depth trawling survey was conducted in 2009 aboard the NOAA ship Henry B. Bigelow to examine pelagic assemblage structure and distribution over the Charlie-Gibbs Fracture Zone (CGFZ) of the northern Mid-Atlantic Ridge. The survey consisted of 11 stations divided into two transects, one northwest and one southeast of the CGFZ, which roughly coincides with the Subpolar Front. Sampling was conducted from 0–3000 m using a Norwegian "Krill" trawl with five codends that opened and closed by a pre-programmed timer. Seventy-five species of fish (29 families, 14 orders) were collected. Maximum species diversity was observed between 700–1900 m. Other key features observed were a strong diel migrating component and frequent

captures of putative bathypelagic fishes in the epipelagic zone (0–200 m). Fish assemblage structure and distribution will be discussed as a function of physical oceanographic features. The results of this expedition have increased our knowledge about oceanic community structure in association with mid-ocean ridge systems and mesoscale circulation patterns.

Biodiversity of sunken wood associated crustaceans (Amphipoda, Isopoda)

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Vegetal organic remains such as wood, plant or macroalgal debris have long been known from the deep-sea floor and the fossil record, with the first reports dating from The Challenger expedition. Sunken wood and plant materials were long time regarded as a mere curiosity, but this is now regarded as a deep sea habitat of biological and evolutionary importance because sunken wood associated fauna are phylogenetically related to those living on hot vents, cold seeps and other organic substrates (whale falls). Relying on a long-term experience in deep-sea exploration, Tropical Deep-Sea Benthos cruises (Mnhn- IRD) aim to improve the knowledge of the bathyal biodiversity in the South West Pacific. Macro-fauna associated to sunken woods was collected during several cruises by using classic fisheries methods (trawling and dredging). In 2004, we started a specific program of cruises focused on sunken woods, providing a large amount of from depths ranging between 100–1500 meters from different locations corresponding to area of most important accumulation of sunken woods: Philippines, Salomon islands, Vanuatu, Madagascar. Biodiversity assessment of sunken wood associated peracarids revealed the recurrent presence of amphipod (Lysianassidae, Melitidae) and isopod families (Limnoriidae, Sphaeromatidae, Cirolanidae). An integrative study has been performed on the Melitidae by combining traditional morphological analyses and molecular taxonomy tools for the identification of the specimens at species level. Specimens from different locations have been identified as belonging to the genus *Bathyceradocus*, and correspond probably to a new species. Microscopic and ultra-structural investigations have confirmed that these specimens are wood-consumers. Moreover, the presence of a probable bacterial ectosymbiosis on the mouthparts and of a resident digestive microflora (bacteria and fungi) suggests original pathways of nutrition involving microorganisms in wood degradation in a possible detoxification with the use in the energetic metabolism.

Thermal stress response of the hydrothermal vent shrimp *Rimicaris exoculata*

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The hydrothermal vent shrimp *Rimicaris exoculata* swarms around black smoker chimneys at most vent sites along the Mid-Atlantic Ridge. This species is believed to occur at the hot end of the hydrothermal biotope in order to provide essential elements to the abundant microbial community that it hosts in its gill chamber, and on which it feeds. Because it is found close to hot venting water, *R. exoculata* lives in a highly fluctuating environment where temperature (2–40°C in the swarms) can exceed its critical maximal temperature (33–38.5 ± 2°C). The aim of this study was to characterize the thermal stress response of *R. exoculata* in order to clarify

the adaptive mechanisms allowing this shrimp to colonize this environment and to specify its thermal optimum. Molecular approaches were therefore conducted on specimens experimented in pressurized aquaria. Several isoforms of heat shock proteins 70 (70 Kda) were identified in *R. exoculata*. Comparison of hsp70 genes expression level of this shrimp with a related coastal species, *Palaemonetes varians*, suggests that *R. exoculata* is rarely exposed to sustained temperature above 30°C in its natural habitat. This hypothesis was also reinforced by the use of a new pressurized recovery device, PERISCOP, which allowed us to access for the first time to shrimps in a physiological state close to natural conditions. In addition, comparison of the different sampling methods (recovery without decompression vs recovery with decompression) allowed us to evaluate the part of the stress response belonging to the decompression effects imposed upon recovery of deep-sea animal. From our in vivo and molecular data we propose that *R. exoculata* thermal preferendum is in the 10–25°C range. An adaptive strategy based on a thermoregulatory behaviour would therefore explain the colonization of this shrimp on black smoker's walls.

Is the Gulf of Cadiz a biodiversity hotspot in the NE Atlantic?

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The deep-sea environment in the Gulf of Cadiz (NE Atlantic) shows a high diversity of benthic habitats including octocoral “gardens”, mostly dead cold water coral reefs, extensive provinces of carbonate concretions, channels and escarpments shaped by tectonic activity and erosion, and over forty known mud volcanoes at depths from 200 to 4000 m. The area is subjected to numerous sources of abiotic and biotic heterogeneity (depth, physiographic and biogenic features, properties of water masses and oceanographic circulation, fluid geochemistry and fluxes of methane and sulphide, surface productivity, etc.) and the seabed supports a high biodiversity. During the past decade, biodiversity studies in the Gulf of Cadiz, contributed to a dataset of over thousand species including both recording of epibiota through in situ surveys (deep-towed video, ROVs) and sampling of sediment fauna. The database has enabled the analysis of species occurrence data using a variety of approaches including regional species accumulation curves. The results are interpreted considering that the surveys were focused on target physiographic features and mostly biased towards the sampling of mud volcanoes and adjacent habitats (carbonate concretions and coral thickets). The number of chemotrophic species (30 species of bivalves and siboglinid polychaetes) recorded from the Gulf of Cadiz is remarkably high when compared to other cold seep regions in the Atlantic and Mediterranean. The majority of these chemotrophic taxa are new to science but our samples also yield new anthozoan, hydrozoan, decapod, tanaid and ophiurid species (published or in preparation), a high “hidden” diversity revealed by molecular approaches in some faunal groups, and a still undetermined number of new taxa of other crustaceans, polychaetes and gastropods. Habitat heterogeneity, oceanographic circulation, the geologic evolution of the region and its biogeographic context are of utmost importance for understanding biodiversity patterns in the Gulf of Cadiz.

14 years of community dynamics at the Atlantic Eiffel Tower hydrothermal edifice

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Since the discovery of hydrothermal vents in the late 1970s, research on these remarkable ecosystems evolved at a quick pace. Although our knowledge of the communities inhabiting these environments has greatly improved, their long-term ecological dynamics remain unclear.

While several time-series studies exist for the Pacific vents, they are extremely scarce for the Atlantic. The present study is the first high-resolution long-term temporal variations study on the Mid-Atlantic Ridge (MAR). Video footage and imagery of 10 cruises (between 1994 and 2008) were analysed for the Lucky Strike vent field. This vent field is situated south of the Azores on the MAR, at a mean depth of 1700 m (37°17.5' N, 32°16' W). Several active hydrothermal edifices are present within this vent field, organised around a central lava lake. The Eiffel Tower sulfide edifice, located in the south-eastern region, is one of the most visited sites and the main focus of this study.

The edifice is dominated by extensive mussel-beds of *Bathymodiolus azoricus*. In association with these mussel-beds live alvinocaridid shrimps, bythograeid crabs and other less conspicuous species. A novel analytical approach was applied to high-definition imagery from Eiffel Tower, yielding insights into small-scale heterogeneity and zonation processes on a MAR vent edifice. Four faunal assemblages and two types of substratum were distinguished based on high-definition photographs and video imagery, and mapped on topographic templates. Community dynamics were investigated on several scales ranging from the entire edifice, between the edifice sides and at small patch scales. Both decadal and inter-annual changes were assessed.

A succession model is proposed and a first quantification of the rate of change in the communities on the slow-spreading MAR showed it was lower than that observed in the communities on a faster-spreading ridge in the NE-Pacific. Despite the changes observed, the overall faunal coverage remained constant between the years.

On wood in the Antarctic, and the fate of shipwrecks

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The southern ocean that surrounds Antarctica is unique in a number of respects. One of these is isolation from other ocean basins as a result of the Antarctic Circumpolar Current (ACC). A second is the lack of regular inputs of woody plant material, which is quite common in all other ocean basins. Large woody trees have been absent from Antarctica since the late Eocene, and the ACC has been in existence for a similar length of time. We decided to test whether specialist wood-fall organisms (teredinid and xylophaginid ship-worms) were present in the Antarctic by deploying wood-fall experiments on the Antarctic shelf. Our experiment

was designed to test two hypothesis, 1) that ship-worm larvae are able to disperse across the Drake Passage and 2) that Antarctica is a preservation ‘vault’ for wooden shipwrecks. We report the results of our experiment.

Mapping the benthic assemblages of Anton Dohrn Seamount

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The UK Deep Sea MPA project was established almost 5 years ago to address where MPAs should be placed within the UK’s deep-sea area in order to achieve representation of known biodiversity. As a contribution to that project a Joint Nature Conservation Committee funded survey was undertaken in 2009 to identify areas of conservation interest and to characterise the ecology of Anton Dohrn Seamount; with the ultimate aim of mapping the distribution of habitats.

High resolution multibeam echosounder data were collected from areas on the NW and SE flanks of the seamount. Video and stills image data were collected from 10 stations, sampling a variety of geomorphological features, substrate types and covering a depth range of 196–1890 m below sea level. 293 images were analysed and epibenthic megafauna identified and quantified. Multivariate analysis of image data identified 13 biological assemblages (biotopes). Video footage was mapped using these biotopes and combined with interpreted acoustic data to produce habitat maps.

The seamount summit was populated with encrusting sponges and serpulids on sandy gravel. Towards the edge of the summit, bedrock provided suitable hard substrate for a number of species, including sessile holothurians, caryophyllids and lamellate sponges. Descending down the flank, this rocky habitat gave way to an area of sand with xenophyophores, which continued to the base of the seamount.

Raised features were found to harbour a number of assemblages of conservation importance. Video footage traversing parasitic cone features revealed the first observation of the OSPAR listed ‘coral garden’ habitat in UK waters. Radial ridges on the NW flank harboured ‘coral gardens’, *Lophelia pertusa* reef and assemblages characterised by small growths of *L. pertusa*, soft corals and glass sponges. Small mounds found on the edge of the seamount summit provided suitable conditions for the growth of *L. pertusa* reefs.

Lanternfish vision: morphological measures of spatial resolving power and sensitivity

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The mesopelagic zone is a relatively dark environment, where the major source of light is emitted by the animals themselves as bioluminescence. Since there is practically no sunlight remaining beyond 200 m, organisms frequenting the mesopelagic zone are subjected to a twilight zone, where the visual system is under tremendous selective pressure. The lanternfishes (Myctophidae) are one of the largest groups of teleost fishes occupying the mesopelagic zone, with a large diversity of species, photophore patterns and vertical migration behaviours. Our study is focussed on visual specializations with respect to light (solar and bioluminescent). The retinae of several species of myctophids were sampled and

preserved for studies of the spatial resolving power and sensitivity of the eye at the level of both the photoreceptors and the ganglion cells. In order to ascertain the level of visual input to the CNS, we have also distinguished the number of neurons not possessing an input to the brain (orthotopic amacrine cells within the ganglion cell layer) using parvalbumin immunohistochemistry and compared them to the ganglion cell population. Initial results indicate that around 20% of neurons within the ganglion cell layer project to the visual centres of the brain via the optic nerve. In the eyes of myctophids, there are several specialisations to enhance sensitivity. These include the tapetum lucidum, a pure rod retina, an increase in rod length and a high convergence ratio of rod photoreceptors to output neurons or ganglion cells. In some genera, a peculiar fundal pigmentation may enhance spatial resolving power on the visual axis. We explore the link between visual specialisations and each species' preferred habitat and behaviour.

Meiofauna of deep-sea cold seeps in the Eastern Mediterranean area, with special emphasis on nematode biodiversity and connectivity

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Seeps are among the most geologically and widely spread of the deep-sea reducing environments. Sulphide provides an unlimited energy source but remains toxic for most metazoans. Microbial mats of sulphide oxidizing bacteria are often formed at the surface of seep sediments where reduced outflows and a source of oxygen are present. Most cold seeps support, compared to more common bathyal environments, highly productive ecosystems characterised by impoverished species richness, a high biomass and an elevated dominance by a few adapted taxa able to survive in high concentrations of the toxic hydrogen sulphide. Megafaunal seep communities and the associated microfauna are relatively well described from a wide number of seep locations from different margins. However, less is known on the biology of small sized endobenthic organisms. Especially meiofaunal studies (< 1 mm, mainly nematodes and harpacticoid copepods) from deep-sea cold seep areas are scarce. Several reduced deep-water environments including mud volcanoes, brine seeps and pockmarks in the Nile fan at the Egyptian margin and on the Calabrian Arc were sampled for meiofauna during the MEDECO Leg 2 campaign (2007), part of the HERMES project, and the Maria Merian cruise (2009, HERMIONE project). The samples collected during these campaigns allow us to get insight in the nematode community structure and biodiversity of the different areas. By sampling both reduced and hemipelagic sediments, it is possible to test if the seep fauna is closer related to the local non-seep fauna than to the taxa found at other seeps from different geographical areas. Molecular studies give insights in the phylogenetic and phylogeographic relationships of seep-nematodes, not only in the Eastern Mediterranean area, but also with more distant seep communities. In general, densities are similar than those found in other deep-sea studies in the Eastern Mediterranean area. A significant difference in genus composition and diversity exists between the reduced and hemipelagic sediments. Hemipelagic samples both from within the seep and outside the seep influence are characterised by a high genus diversity and were dominated by more typical deep-sea genera like *Acantholaimus*, *Halalaimus*, *Thalassomonhystera*, *Microlaimus*, *Theristus* and *Tricoma*. The nematode assemblages from the reduced sediments of all cold seep sites are genus-poor, and strongly dominated by the genus *Sabatieria* (*mortenseni*), which is also the dominant genus in the REGAB cold seep adjacent to the Congo canyon in the Gulf of Guinea

(Equatorial West-Africa, South Atlantic). It can be concluded that seep sediments which are strongly affected by reduced fluids, generate a habitat which is difficult to colonize by most of the typical deep-sea nematode species. Apparently, dominant nematodes from these isolated habitats are often cosmopolitan eurybathic species with very high tolerance levels. The presence of *Sabatieria (mortenseni)* as prevailing species in different remote seeps can indicate a possible interconnection. In order to gather deeper insights in this topic it was already possible to extract DNA from these deep-sea nematodes present in the cold seeps. Next to this, parts of the nuclear DNA were sequenced successfully. Further molecular investigations in the next months can give more answers concerning this topic.

Kaikoura submarine canyon, East New Zealand Margin: an oasis of food for deep-sea benthic communities

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Submarine canyons are dramatic and widespread topographic features crossing continental and island margins in all oceans. Canyons can be sites of enhanced organic matter flux through entrainment of coastal detrital export, dense shelf water cascade, channeling of resuspended particulate material, and focusing of sediment deposition. Despite their unusual ecological characteristics and global distribution, only scattered information is available about the influence of submarine canyons on deep-sea ecosystem structure and productivity. Here we show that deep-sea canyons such as the Kaikoura Canyon on the New Zealand margin can sustain enormous biomasses of infaunal megabenthic invertebrates (holothurians such as *Molpadia musculus*, the echiuran *Alomasoma nordpacificum*, and maldanid polychaetes) over large areas. Our reported biomass values are 100-fold higher than previously reported for deep-sea (non-chemosynthetic) habitats below 500 m in the ocean. We also present evidence from deep-sea towed camera images that areas in the canyon which have the extraordinary benthic biomass also harbor high abundances of macrourid fishes likely to be feeding on the macro- and megabenthos. Bottom-trawl data also indicate that Kaikoura Canyon has dramatically higher abundances of benthic-feeding fish than adjacent slopes. Our results demonstrate that Kaikoura Canyon is one of the most productive habitats described so far in the deep sea. A global tabulation of submarine canyons suggests that there are of order 100 canyons worldwide with physical/oceanographic characteristics similar to Kaikoura Canyon that are potentially intense hotspots of biomass and fisheries production.

Metabolism of demersal fishes from the eastern North Pacific

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Many studies of deep-sea animals have documented feeding habits as well as regional and depth related patterns in biomass, abundance, and community composition. The void in studies of deep-sea benthic communities is information on metabolic rates. Metabolism sets the pace of many processes such as resource utilization, growth, and reproduction that in scales up to control many ecological processes. Our lack of rate information has been an obstacle to constructing dynamic food webs. Available data for pelagic animals, some of

which show dramatic declines with depth, forms the basis of the Visual Interactions Hypothesis (VIH). It suggests that metabolic declines occur due to declining light levels which reduce the reactive distances of visually orienting animals. The VIH suggests that declines in metabolism will only occur in predominantly pelagic species. To test this hypothesis we have developed an autonomous in situ respirometry system that captures demersal fishes to measure their metabolism via oxygen consumption. Measurements on five species from 1000 to 3000 meters were made. Benthopelagic species (those that swim in the water column above the seafloor) had rates roughly an order of magnitude lower than their shallow water relatives. Benthic species (those that commonly rest on the seafloor) had rates similar to their shallow living relatives. These results were augmented by laboratory measurements for two species of hagfishes. In situ and laboratory measurements were similar, suggesting that decompression of the deeper living species had little or no effect on whole animal metabolism. The rates for the shallow and deep living species were also similar. These results generally support the VIH in that swimming species exhibited declines and benthic species, as well as blind hagfishes, showed no depth related variation in metabolism. Augmentation of respirometry measurements by assays of key enzymes of intermediary metabolism will be discussed.

Orange roughy fisheries around New Zealand; the first and last?

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This paper describes recent problems, and progress, in assessing and managing the orange roughy stocks around New Zealand. The New Zealand orange roughy fisheries have been the largest and most persistent in the world. Stock assessment models have been used to set catch quotas for optimal and sustainable exploitation of stocks. However the stock assessment models have failed to explain much of the observational data and, despite low catch levels, some stocks have apparently continued to decline. This suggests the models are wrong. Problems with the models include fitting the steep initial decline seen in biomass indices, which are too steep for them to be true indices of stock abundance; mismatches between the estimated age of recruitment and selectivity, suggesting some mature fish are always unavailable to fishing (so called “cryptic biomass”); and estimating productivity and recruitment, which remains difficult because ageing of orange roughy is imprecise. As a result of the poor model fits to observational data, the stock assessment model for the largest fishery, on the east Chatham Rise, was abandoned in 2008. In its place, an alternative stock assessment and management method based upon taking a fixed proportion of the spawning plume was introduced. Nevertheless, there remains a pressing need to solve the problems with the stock assessment models, and thereby to understand how orange roughy populations work. For this to happen, biologists first need to develop new ideas and hypotheses. Despite calls to close many orange roughy fisheries, if science can understand orange roughy then sustainable New Zealand fisheries should be attainable; a recent survey of the Challenger Plateau stock, which was closed to fishing in 2001, found substantial spawning plumes and suggests that when fishing mortality is reduced, biomass rebuilds are possible.

An overview of deep-sea mussel symbioses: facts, hypotheses and future directions

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Bacterial symbiosis is a shared feature of all mussels thriving at deep-sea chemosynthesis-based ecosystems (seeps, vents, organic falls). Symbiosis has been documented in 27 species: 17 harbour only sulphur-oxidizing (SOX) Gammaproteobacteria, 3 harbour only methane-oxidizing (MOX) Gammaproteobacteria, and 7 harbour multiple symbioses. Five of the latest harbour dual symbioses (both SOX and MOX), and 2 harbour symbioses involving more partners. A good overview of mussel symbioses is thus becoming available, and general features as well as evolution of these associations can now be discussed. Symbionts occur in or on gill epithelial cells, and contribute significantly to carbon uptake. Although specific, associations are flexible with regards to symbiont abundances and at least SOX acquired anew from the environment at each generation. Although hosts and bacteria do not co-speciate, closely related hosts tend to harbour closely related bacteria. Besides, it can be hypothesized that the capacity to establish associations with a clade of SOX bacteria was present in the latest common ancestor of deep-sea mytilids. This capacity probably opened new niches, and could have triggered a radiation of the group that translated into the large multifurcation observed in host phylogenies. Associations with a MOX clade, and other bacteria, seem to have appeared several times independently. Extracellular SOX were discovered in vent- and wood-associated species. However, no self-evident pattern of evolution from extra- to intracellular symbioses yet appears in host or symbiont trees. Although good phylogenies are becoming available for hosts, more detailed symbiont phylogenies are needed to document symbiont evolution and biogeography. Free-living forms of symbionts should be searched for. Investigation of symbiont genomes will give insights into their true capabilities, as associates or free-living bacteria. Finally, in situ monitoring as well as ex situ experimentation are mandatory to really understand the functioning of “symbiotic systems” formed by mussels and their symbionts.

Species-specific carbon uptake by an abyssal foraminiferal community during a simulated phytodetrital pulse in the North Pacific

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Foraminifera are a diverse and ecologically important meiofaunal group in deep-sea sediments. Like other inhabitants of the abyssal region, they largely depend on sinking particulate organic matter as energy source. This material is generated in the surface waters during phytoplankton production and reaches the seafloor in pulse-like events. To investigate the role of the benthic deep-sea community within the global carbon-cycling, it has been successfully demonstrated that feeding experiments at the sea floor using isotopic tracers are an useful tool. In this study we investigated living benthic foraminifera at Station M (34°50'N, 123°00'W, 4100 m depth) in the North-East Pacific and assessed their response to a simulated phytodetrital pulse during a short-term in situ experiment. Oceanlab spreader

systems were deployed at the sea floor with a ROV and enclosed sediments were incubated with ^{13}C -labelled *Thalassiosira weissflogii* (Bacillariophyceae), a characteristic phytoplankton species of the region. After four days, two sediment cores containing tracer material and additional unlabelled background sediments were recovered for isotopic and faunal analyses. The living foraminiferal community is dominated by soft-shelled foraminifera with relative abundances in deeper sediment layers of up to 71%. The agglutinated foraminifera showed the highest diversity within the assemblage (about 60 taxa) with a high portion of epifaunal species (e.g. *Rhabdammina abyssorum*, *Adercotryma glomeratum*) whereas calcareous taxa were of minor importance. Abundances of living foraminifera at the sediment surface are significantly higher as within the sediment. After the 4 d incubation period, about half the foraminiferal species showed an uptake of the labelled phytodetritus with considerable differences between and within taxa. Epifaunal species demonstrated the highest $\delta^{13}\text{C}$ values at the sediment surface while other species displayed $\delta^{13}\text{C}$ maxima at greater depths (e.g. *Hormosinelloides guttifer*) or did not show any algae ingestion (e.g. *Melonis barleeaanum*, *Uvigerina auberiana*). Despite clear signs of vitality and a strong representation in the foraminiferal community, none of the soft-shelled taxa showed a noticeable response to the offered algal material. Selective food preferences, as observed for other foraminiferal species, might explain the apparent reluctance to consume the offered *T. weissflogii*. As typical inhabitants of abyssal sediments, soft-shelled foraminifera might be adapted to the consumption of more degraded organic matter.

Evolution in the deep Atlantic inferred from the phylogeography of an abyssal protobranch bivalve

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We know very little about how the deep-sea fauna evolved. Even basic questions about the scales and geography of population divergence are poorly understood, especially for abyssal organisms. Although we have made some progress in understanding evolutionary processes at bathyal depths, much less is known about geographic or bathymetric patterns of genetic variation at abyssal depths. Here we quantify the geographic and bathymetric patterns of genetic variation in the protobranch bivalve *Ledella ultima*. *Ledella ultima* is one of the most abundant abyssal protobranchs in the Atlantic with a broad bathymetric and geographic distribution. Ocean-wide patterns of genetic variation indicate basin wide divergence that exceeds what others have found for abyssal organisms, but muted compared to bathyal protobranchs across similar geographic scales. Levels of population divergence among basins are greater in the South Atlantic than in the North Atlantic. Demographic inferences based on genetic variation indicate abyssal populations began a slow and steady expansion over the last million years with estimates of contemporary effective population size within basins exceeding 1 million individuals. Migration rates across the North Atlantic appear to be strongly asymmetric with greater dispersal from the eastern to the western North Atlantic. Our results indicate that abyssal populations might be quite large, exhibit genetic divergence at ocean-wide scales, and probably evolve at a much slower pace than bathyal species.

Reproductive patterns in pelagic decapod shrimps from the Northern Mid-Atlantic Ridge

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Decapod shrimps comprise a significant part of the micronekton biomass in the mesopelagic zone of the oceans. The accumulated information on their distribution, migration and life histories suggests that pelagic shrimps play important roles in the vertical transport of organic matter in the oceanic system. Knowledge on their distribution and population structure is necessary to understand their role in the pelagic ecosystem. We present reproductive patterns and population characteristics of three species of mesopelagic decapod shrimps sampled along the northern Mid-Atlantic Ridge (MAR; Iceland to the Azores) on a survey conducted as a part of the Census of Marine Life field project MAR-ECO. Ovarian maturation, embryogenesis and fecundity is described for *Parapasiphae sulcatifrons*, *Acantheephyra pelagica* and *A. purpurea*.

P. sulcatifrons has few, large eggs and morphologically advanced larvae at hatching, while the two *Acantheephyra* species produce numerous small eggs, hatching as planktotrophic, early larvae. This demonstrates that different reproductive strategies are present in co-occurring species in the deep-sea. The observed results are discussed in relation to vertical and latitudinal variations in environmental factors.

Trophodynamics of deep-sea macrozooplankton and micronekton off the Catalan slope: insight from stable isotopes

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Food web structure of the macroplankton/micronekton fauna on the continental slope of the Catalan Sea (Balearic basin, NW Mediterranean) was investigated using carbon and nitrogen stable isotope tracers on a total of 33 taxa. Samples were collected close to Barcelona, Spain, between 650 and 800 m depths, at a seasonal scale, from January 2007 to February 2008. Mean $\delta^{13}\text{C}$ values ranged from -22.1‰ (*Salpa maxima*) to -16.9‰ (the mysid *Eucopia hansenii*). Values of $\delta^{15}\text{N}$ ranged from 2.5‰ (the hyperiid *Vibilia armata*) to 9.8‰ (the pelagic polychaete *Tomopteris* sp.). The stable isotope ratios of this fauna displayed a continuum of values over the $\delta^{15}\text{N}$ range of 7‰ , confirming a wide spectrum of feeding strategies (from filter feeders to predators). High annual mean $\delta^{15}\text{N}$ values were found among carnivorous large zooplankton and micronekton, including species that prey on gelatinous plankton, euphausiids, natantian decapods and mesopelagic fish. In agreement with the available information on diets of planktonic taxa, the lowest isotope ratios were found for filter feeders (hyperiid, salps, pteropods, ostracods and thaliaceans), all of which feed on POM. We found three trophic levels in macroplankton/micronekton food webs based on an ^{15}N -enrichment factor of 2.5‰ per level. The range of $\delta^{13}\text{C}$ was particularly wide among carnivores (-20.7‰ to -16.6‰), suggesting predation on a variety of prey from gelatinous zooplankton (which displayed more depleted $\delta^{13}\text{C}$ signatures) to small fishes and decapods. Correlation between $\delta^{13}\text{C}$ - $\delta^{15}\text{N}$ was generally weak, likely due to the consumption of different kinds of sinking particles, some constituted of multiply recycled POM. However,

higher $\delta^{13}\text{C}$ – $\delta^{15}\text{N}$ correlations were observed during winter and spring, periods of water column homogenization, suggesting that the planktonic community assimilates pulses of new production from the photic zone. Low correlations were observed during periods of water column stratification, particularly in summer, when production is especially low.

Distribution and reproductive biology of deep-sea grenadier fish (Family: Macrouridae) from the northwestern Mediterranean Sea

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The present study is an analysis of seasonal and depth-related trends in abundance, biomass, body size and reproductive strategies of four grenadier species *Coelorinchus mediterraneus*, *Coryphaenoides guentheri*, *Nezumia aequalis*, and *Trachyrinchus scabrus* of the deep western Mediterranean. The specimens were obtained using an OTMS bottom trawl along a seasonal period (autumn 2008 - autumn 2009), inside and outside the Blanes Canyon (Catalan Sea) at depths between 900 m and 2000 m. These species present a different depth range distribution: *Nezumia aequalis* and *Trachyrinchus scabrus* show its maximum in abundance and biomass at upper slope (900–1050 m), *Coelorinchus mediterraneus* at middle slope (1200–1500 m) and *Coryphaenoides guentheri* at lower slope (1500–2000 m). Size trends varied depending on the species. Females grow larger than males and, except for *Coelorinchus mediterraneus*, females outnumbered males. The Mediterranean Sea is a physically fairly constant and oligotrophic environment. Hence, we might expect a consistent pattern of reproduction of all the above-mentioned species. In contrast, the macroscopic and microscopic analyses of the gonads exhibit different reproductive strategies within the macrourid family, which vary between continuous (*Nezumia aequalis*), quasi-continuous (*Coelorinchus mediterraneus*) and seasonal (*Trachyrinchus scabrus* and *Coryphaenoides guentheri*) reproductive cycle. The adoption of different reproductive strategies is probably related to avoid competence between these species for the same trophic resources. Moreover, our results indicate that the main reproductive period is from autumn to winter, coinciding with the formation of mixed layers in the Mediterranean Sea. This further corroborates the hypothesis that reproductive periods in deep-sea fish have adapted to fluxes of organic matter from the photic zone. Further analyses of additional species belong to the same deep-sea community (e.g. Moridae and Notacanthidae) and the characterization of the environmental conditions will help us in finding the existence of a general demographic and reproductive pattern and identifying the underlying environmental factors.

A comparison of bacterial diversity in two contrasting tubeworm habitats

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Hydrothermal vent communities are subject to great spatial and temporal variations of environmental conditions, affecting their distribution by creating diverse habitats. However, little is known about how vent habitat conditions affect the free-living microbial communities, which represent the basis of the food webs in this ecosystem. Our study investigated the

structure and diversity of the free-living bacterial communities inhabiting the substratum within aggregation of the tubeworm *Ridgeia piscesae*. This vestimentiferan is the major foundation species of the Endeavour Hot Vents marine protected area (MPA), located on the Juan de Fuca Ridge, approximately 200 km off the west coast of Canada. Samples of *R. piscesae* were collected from high-flow and low-flow diffuse venting sites. Microbial DNA was extracted from the particulate debris associated with the tubeworms. We used small subunit ribosomal RNA (SSU rRNA) gene sequence data to compare the composition of the bacterial communities in the two contrasting tubeworm habitats. The results show a greater phylogenetic diversity at low flow sites, where the conditions are milder and the tubeworms are in poor condition. In contrast, bacterial groups related to the sulphur cycle (primarily Epsilonproteobacteria) dominated clone libraries from the high flow sites, where the tubeworms were in good reproductive condition.

Spatial heterogeneity of megafaunal communities related to fluid seepage in the Niger delta

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The structure and distribution of the benthic megafaunal communities were investigated on different seafloor features in the Niger delta within the framework of a joint research project between Ifremer and the oil company TOTAL. Visual observations (videos and photos) of the bottom were obtained by a towed camera on selected areas where available data suggested the occurrence of fluid seepages. Between 450 and 1630 m depth, different types of geological structures were investigated including three pockmarks, one mud large mud volcano and one compression area. In the pockmark areas muddy sediments were interspersed with carbonate crusts and methane hydrates could be present in subsurface layers. The mud volcano showed a prominent dome and heterogeneous substrates varying from soft sediment to rocks, boulders or carbonate debris and concretions. The compression area was characterized by clay mounds and small diapir-like structures. The benthic megafaunal communities associated with the different geological settings and types of substrate are described, and the relation between the community structure and habitat is tested. New types of communities linked to methane seepage were recorded for the first time in the Gulf of Guinea. These communities are dominated by sponges among which several morphospecies are recognized. Mytilid and vesicomid bivalves together with siboglinid worms are the other main components of these chemosynthetic communities.

CHEMECO (Colonization processes in CHEMosynthetic ECOsystems) Eurodeep ESF: a synthesis

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The discoveries of new types of ecosystems on mid-ocean ridges and continental margins have changed our vision of biodiversity into the deep-sea. The energy supply to these communities rely on methane- and sulphide-oxidizing microaerobes which are unique in their ability to satisfy their carbon and nitrogen needs from inorganic sources, under free-living forms or symbiotic association with invertebrates. Geologically-driven sources of such reduced compounds to the deep-seafloor (hydrothermal vents, methane seeps) are mostly ephemeral and discretely distributed, such are massive organic inputs (whale carcasses, sunken woods) that harbour species closely related to vent and seeps endemic taxa. These fragmented reducing habitats, however, markedly differ in their chemical/biogeochemical features and temporal dynamics. The aim of the CHEMECO project was to gain information on the biological, microbial, biogeochemical, and ecological aspects of mineral and organic substrates colonisation by metazoans in reducing habitats. Focuses were first on the establishment of pioneer microorganisms (prokaryot and eukaryot) communities using stable isotopes, lipid biomarkers, anaerobic culture under pressure and sequencing techniques, secondly on the recruitment of metazoan larvae using classical microscopic techniques, in situ hybridization or DNA sequencing (18S, COI, ITS2, 16S), the development of symbioses and trophic structure of newly-established communities. We addressed these issues through a unique combination of site surveys (1) MoMAR hydrothermal sites on the Mid-Atlantic Ridge (Rainbow and Lucky Strike), 2) Håkon Mosby mud volcano (HMMV) in the Norwegian sea, 3) Nile deep-sea fan brines and seeps areas in the eastern Mediterranean, 4) Mercator, Meknes, Darwin and Carlos Ribeiro Mud Vulcanoes in the Gulf of Cadiz, 5) one shallow site into the west-Atlantic ocean coastal area (Caribbean islands), all of them using in situ colonization experiments (CHEMECOLI: (CHEMosynthetic Ecosystem COLonization by Larval Invertebrates), and monitoring with microsensors. This paper will address a synthesis of this multidisciplinary approach.

Amphi-Atlantic chemosymbiotic mussel species “*Bathymodiolus*” *mauritanicus*: insights into larval dispersal using physical modeling

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Chemosymbiotic mussels are distributed in hydrothermal vents and cold-seeps worldwide. The “*Bathymodiolus*” *childressi* clade is the most geographically diverse assemblage of deep-sea mussels, being found in the West Pacific and also, in the East and West Atlantic. *Bathymodiolus* mussels were collected for the first time in the Gulf of Cadiz (NE Atlantic) in 2006. Morphological observations of shell features indicate that they belong to the “*B.*” *childressi* species complex, which has been recognized morphologically and genetically distinct from the other *Bathymodiolus* species. Molecular analyses show that the Gulf of Cadiz mussels and other analyzed specimens from Barbados are conspecific with “*Bathymodiolus*” *mauritanicus* Cosel, 2002, described from West African margin, supporting a previous hypothesis that “*B.*” *mauritanicus* is an amphi-Atlantic species. Larval dispersal is a key factor influencing population dynamics of marine species. The combination of multiple approaches, including genetic and environmental markers, and also physical modeling, has provided new insights into population connectivity of marine coastal areas. However, application of these methodologies in the deep-sea still faces many challenges. Here we present preliminary results from a series of simulations using a numerical model developed for the Gulf of Cadiz (GoC) attempting to elucidate the distance and directions of larvae movement of the chemosymbiotic mussel species. Although little is known of the larval biology of “*Bathymodiolus*” *mauritanicus* recent studies on the closely related species “*Bathymodiolus*” *childressi* have provided the behavioral parameters for the model simulations: spawning season (October to February) synchronized with the peak of water productivity; larval development (planktotrophic); larvae survival (2–8 months, maximum up to 13 months). So far, the results of this study are promising and further research may be used to constrain null hypotheses for connectivity studies of deep-sea chemosynthetic populations.

Meiofauna associated with cold-water corals: composition, diversity and adaptation

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Cold-water corals are one of the most three-dimensionally complex habitats in the deep ocean. Nearly all studies on the associated macro- and megafaunal communities of these reefs indicate a high biodiversity which rivals the diversity of tropical zooxanthellate coral reefs. Our recent work in the Belgica Mound area of the Porcupine Seabight (Northeast Atlantic) has described the associated metazoan meiofauna of coral rubble and associated microhabitats. Attention was focused on the influence of microhabitat type on assemblage structure and diversity. Coral rubble provides a coarse substrate that hosts specific faunal taxa and lifestyles. Compared to their underlying sediment environments, dead fragments of the coral *Lophelia pertusa* and the glass sponge *Aphrocallistes bocagei* were characterised by significantly lower nematode densities and higher densities of other taxa such as harpacticoid copepods. The harpacticoid copepod community included typically epifaunal taxa with distinct morphological adaptations to the specific conditions of this habitat. Certain genera

(such as *Halophytophilus* and *Tegastes*) were recorded for the first time from the deep sea, which is an indication that the hard substrates of the coral degradation zone provide an exceptional habitat compared to the surrounding soft-bottom deep-sea floor. At least 80% of the 157 harpacticoid species recognized were considered new to science. There are clear indications that the harpacticoid assemblages in cold-water coral degradation zones are highly diverse, in terms of species richness as well as equitability, and might even be more diverse than in tropical coral degradation zones. On a small spatial scale, the presence of coral rubble and associated microhabitats at the ocean margins greatly influences the meiobenthic community living in close association with *Lophelia* reefs.

New discoveries of whale-fall fauna from deep water off Antarctica and Southern California

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Using a new experimental approach we have successfully recovered new species of the bone-eating worm, *Osedax*, from shelf-depth (approx 500 m) sites in Antarctica. This extends the biogeographic range of this recently-discovered clade of siboglinid polychaetes into waters south of the Polar Front. We also report on another new species of *Osedax* from a whale-fall in the Santa Cruz basin, NE Pacific, and a new record of *Osedax frankpressi* Rouse et al. 2004 from a site close to San Clemente, NE Pacific. We explore the morphology and molecular phylogenetic relationships of these new *Osedax* species and discuss biogeographic patterns and the issue of dispersal between isolated whale-fall sites.

Benthic food web interactions in the deep Faroe-Shetland Channel: combining stable isotope labelling with linear inverse modelling techniques

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Stable isotope labelling experiments have allowed the direct observation of the transfer of fresh phytodetritus through food webs. The pulse-chase methodology enabled the quantification of the contribution of particular species to the processing of fresh organic matter and revealed various benthic response patterns to organic matter enrichment. Despite the significant progress in unravelling trophic interactions using labelling techniques, it is impossible to measure directly the full range of flows that exist in complex food webs. The linear inverse modelling (LIM) methodology was developed in order to overcome these data limitations and quantify biological interactions in complex food webs from incomplete and uncertain datasets. However, several issues have emerged regarding the selection of the “best” food web using optimization criteria that lack an ecological basis. Tracer flow data, as revealed by labelling experiments, can be used as a measure of the “best” food web solution

based on field data. We combined the LIM methodology with a high-quality dataset consisting of biomass, oxygen flux, background $\delta^{15}\text{N}$ signatures of consumers and isotope tracer data to analyse food web interactions in a deep-sea benthic community. The data stemmed from sampling and experimental work in the Faroe-Shetland Channel. The high taxonomic resolution of the macrofaunal community analysis enabled the construction of a detailed food web and the quantification of the flow of energy between detrital compartments, bacteria, meiofauna and the major macrofaunal taxa and polychaete functional groups.

Composition and structure of mytilid-based assemblages on hydrothermal fields in the Atlantic and Pacific Oceans

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Bivalve mollusks of the genus *Bathymodiolus* (Mytilidae) are widely distributed at hydrothermal vents in the Pacific, Atlantic and Indian Oceans. Mussel beds are colonized by diverse assemblages of macrofaunal and meiofaunal invertebrates. Mytilid assemblages generally occur at moderate diffuse flow regimes with temperatures up to 10°C. The aims of present study were: to investigate the variability of structure of mytilid assemblages between hydrothermal sites along mid-ocean ridges in the Atlantic and Pacific, to analyse similarity between mytilid assemblages at hydrothermal vents on the East-Pacific Rise (EPR) and on the Mid-Atlantic Ridge. Original and published quantitative data on mussel-based assemblages were summarized. In the Atlantic, assemblages dominated by *Bathymodiolus azoricus* were investigated at Menez Gwen, Lucky Strike and Rainbow; assemblages dominated by *B. putheoserpentis* - at Broken Spur, Snake Pit and Logatchev. In the Pacific (EPR), assemblages dominated by *B. thermophilus* were investigated at 9°N (hydrothermal fields Biovent, East Wall, Train Station and Mussel Bed), 11°N and 17°S (Animal Farm, Oasis, Rehu Marka). Original material was collected using submersibles Mir on cruises of the RV Akademik Mstislav Keldysh at Menez Gwen, Lucky Strike, Rainbow, Broken Spur, Snake Pit and 9°N EPR. Taxa richness, composition of dominant taxa, rank abundance patterns, diversity, evenness of assemblage structure and abundance of meiofauna were estimated at each site. Comparative analysis of these parameters revealed significant differences between Atlantic and Pacific assemblages. Atlantic assemblages are characterized by high variability in structure between vent sites. Differences between assemblages dominated by *B. azoricus* and *B. putheoserpentis* in the Atlantic are more prominent than differences between *B. thermophilus* assemblages at northern and southern EPR vent fields.

The trophic ecology and colonization capacity of deep-sea nematodes: experimental evidence

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At the Arctic deep-sea observatory HAUSGARTEN (79°N 5°E, west of Svalbard) 2 experiments were performed in order to gain insight on the trophic ecology and the colonization capacity of deep-sea nematodes. At first, an on board stable isotope (^{13}C)-labeling experiment was performed to quantify the importance of bacterial carbon as food source for the Arctic deep-sea nematode community. Therefore the substrates ^{13}C -glucose, ^{13}C -acetate, ^{13}C -bicarbonate and ^{13}C -amino acids were injected into sediments collected from a 1280 m slope station. Incorporation of the ^{13}C label into bacterial phospholipid-derived fatty acids (PLFAs) and nematodes was monitored over a 7 day period, after which the ^{13}C dynamics of nematodes were fitted with a simple isotope turnover model. To jump to the conclusion bacteria do not seem to be important as carbon sources for the nematode community. The second experiment was performed in situ at 2500 m depth. 500 μm -mesh-coated cylinders filled with only azoic sediment or azoic sediment with different ^{13}C -labeled food sources (diatoms and bacteria) were inserted in the sediment by means of the ROV Quest. After 10 days of incubation the cores were retrieved. Results show that nematodes actively colonized both the enriched and the unenriched sediment, with certain species showing more efficiency, regardless however of the presence and the type of food. As nematodes neither showed uptake of the ^{13}C -labeled diatoms and bacteria in this experiment, the food sources of deep-sea nematodes remain an enigma.

Temporal and spatial dynamics of mesopelagic macroplankton

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Although the deep water-column is the largest habitat on earth, we are only just discovering many of its inhabitants. Merely sampling them is a difficult endeavor, but even more challenging is understanding how the abundances and distributions of these diverse organisms change over time. Nevertheless, it is important to examine these patterns in order to understand potential changes that may be occurring in the sea. Using a 20-year video record of animals in the eastern north Pacific, we have assembled time and depth data for representatives from major taxonomic and trophic groups. Some species show remarkably constant distributions over time, while others fluctuate in correspondence with El Niño and other dynamic components of the environment. Some species have narrowly restricted depth ranges, while others can even have bimodal distributions. Despite the relative constancy of the environment, fluctuations in deep-sea pelagic communities can still be detected.

The evolutionary history and phylogeny of the sub-family Lithodinae (Decapoda: Anomura: Lithodidae)

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The king and stone crabs of the family Lithodidae include some of the largest arthropods currently inhabiting the oceans. They have a cold-water distribution, tolerating temperatures between 1 and 12°C, and are predominantly encountered in waters between 300 and 3000 m deep, and in shallower waters at high latitudes. It has been proposed that king crabs emerged relatively recently (within the last 20 million years) from an anomuran group in the shallow waters of the North Pacific. Molecular evidence suggests some ancestral connection with the *Pagurus* genus. If previous molecular-based estimates prove to be true, then the current worldwide distribution of the Lithodinae is the result of a rapid radiation through the deep-sea. This is even more significant considering that several groups of Lithodinae have been shown to have larvae, which are demersal drifters rather than actively swimming planktonic stages. In the current study, we use evidence from 5 genes (COI, 16s, 28s, COII, ITS) and over 100 morphological and morphometric characters to explore the relationships between the widespread sub-family with the aim of elucidating the temporal and geographical scales of evolution through the deep-sea. We have examined the genetic and morphological nature of species on a local scale, to indicate that a degree of hybridisation and/or morphological plasticity occur between closely situated groups. In addition, we have looked at the pathways of spatial radiation indicated by phylogenetic reconstructions to assess the likelihood of such rapid radiations occurring within a short timescale as has previously been suggested.

Impact of macrofauna bioturbation on small-scale distribution patterns of deep-sea meiofauna: an experimental approach

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To investigate the impact of small-scale environmental changes on meiobenthic community structure a short-term in situ experiment was carried out to examine and monitor factors controlling deep-sea diversity. In order to understand the complex interactions between the biota (their functioning and diversity) and environmental perturbations/relaxations a free-falling device (bottom lander) equipped with sediment disturber (SD) has been used. This in situ technology will provide scientific insight to effects on the sediment geochemistry and associated benthic fauna, due to repeated disturbances (e.g. as caused by bioturbating megafauna). This will allow the investigation of shifts in community structure of the small sediment-inhabiting biota in response to perturbations and changing chemical condition of the deep-sea sediment. The SD was deployed at the central HAUSGARTEN station (79°4.48'N 4°8.58'E, 2493 m water depth) for nine days. The SD carries three rotating fork-like disturber units able to perturbate the upper sediment layers at chosen time intervals. Three disturbed areas were created by the SD with different disturbance frequencies of four (disturber unit I), two (disturber unit II) and one disturbance (disturber unit III) within nine days. A camera system continuously monitors all SD actions. Sediment sampling at the end point of the deployment has been carried out using push-coring devices handled by the ROV "Quest 4000". With the manipulator arm of the ROV three sediment cores have been taken from each

disturbed area. In front of each disturbed area two background samples have been taken outside the SD footprint. The sediment cores have been sub-sampled to study the effect of controlled sediment perturbations on biochemical sediment parameters as well as on benthic meiofauna communities (with special focus on nematode communities). We will present first results of nematode abundances in the upper sediment layers.

Depth-abundance and depth-size relationships for deep-living nekton in the mid North Atlantic

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During the 2004 cruise to the Mid-Atlantic Ridge between Iceland and the Azores with RV G. O. Sars, two pelagic trawls, the macrozooplankton and the Åkra trawl, were used. These were equipped with multiple codends that enabled covering the entire water column during a single haul, while still obtaining samples from specific depth ranges. Combining data from these trawls, we present detailed depth profiles of abundance and mean size for common pelagic fishes, cephalopods, decapods and jellyfish. The data reveal that (1) subtropical submergence is common, in particularly fishes, and that (2) if there is a relationship between mean individual size and depth, this tends to be positive.

The deep sea coral research and technology program: research to conserve biodiverse deep-sea ecosystems

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NOAA National Marine Fisheries Service, Office of Habitat Conservation
NOAA National Marine Fisheries Service, Northwest Fisheries Science Center
NOAA National Marine Fisheries Service, Southeast Fisheries Science Center
NOAA National Ocean Service, National Centers for Coastal Ocean Science

Deep-sea corals and sponges can form complex biogenic habitats of astonishing biological diversity. Before most areas have even been surveyed, however, these deep-sea communities are threatened by damage from fishing gear and other activities. In 2009, the United States National Oceanic and Atmospheric Administration (NOAA) launched the Deep Sea Coral Research and Technology Program, called for in the reauthorization of the Magnuson-Stevens Fishery Conservation and Management Act, the nation's primary fishing law.

The Program conducts targeted field expeditions using state-of-the-art mapping and research technologies, and analyzes and integrates existing information on the deep-sea coral ecosystems and human activities that may impact them. Initial Program priorities are to identify and map deep-sea coral habitats and understand their relationship to fisheries species and biodiversity. Although targeting deep-sea coral ecosystems within the U.S. EEZ, the Program can serve as a U.S. partner for international collaborations such as the proposed Trans-Atlantic Coral Ecosystem Study and efforts to identify and protect vulnerable marine ecosystems.

In its first year, new mapping and exploration in deeper waters off Florida identified new coral-rich areas that informed the final boundaries in the South Atlantic Fishery Management

Council's historic efforts to enhance protection for over 62,000 square kilometers of seafloor containing complex deepwater coral habitats off the coasts of the Carolinas, Georgia, and eastern Florida. In 2010, the Deep Sea Coral Research and Technology Program is expanding new field research to the U.S. West Coast, in partnership with the region's five National Marine Sanctuaries and the Pacific Fishery Management Council. This talk will report on the Program's first year of activities, map out future plans and identify the national and international partnerships that can link this research to improved understanding and management of these important ecosystems.

Mating tactics in deep-sea squid

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Squid are pelagic marine molluscs that are increasingly important components of marine foodwebs. Most squid, in both biomass and number of species, live in waters below 200 m of depth. Despite the ecological success of deepwater squid, their physiology and behaviour remains poorly known. Observations on living deep-sea squid are rare and require sophisticated technology. Research on these animals therefore still mainly happens via the examination of dead animals. As part of my PhD research I have studied the reproductive biology of several species of deepwater squid, which were caught by bottom- and midwater-trawl, or retrieved from predator stomachs. In my talk I will focus on the mating tactics (reproductive morphology, sperm transfer and sperm storage) that are present in deep-sea squid. I will present an overview of the recently discovered mechanisms that deep-sea squid possess to ensure successful transfer and storage of sperm. Species that were investigated range from the small bobtail squid *Heteroteuthis dispar* (mantle length 25 mm) to the giant squids *Architeuthis* and *Taningia danae*.

Mapping the deep - the UK's deep-sea marine protected area network project

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Joint Nature Conservation Committee
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British Geological Survey

Internationally there is political momentum to establish networks of representative Marine Protected Areas (MPAs) for the conservation of biodiversity. Almost 5 years ago the UK Deep Sea MPA project was established to address the very basic question of "where should MPAs be placed within the UK's deep-sea area in order to achieve representation of known biodiversity?" The submarine features of the UK's deep-sea area: Hatton Bank, George Bligh Bank, Rockall Bank, Anton Dohrn Seamount, Rosemary Bank Seamount, the Wyville-Thomson Ridge, the Faroe-Shetland Channel, and Dangaard and Explorer Canyons, have been surveyed over a four year period (2005–2009) using a combination of multibeam and sidescan sonar acoustic data, ground-truthed with video and stills imagery. More than 30,000 km² of acoustic data have been interpreted, and 226 videos and associated stills images, totalling more than 120 km of seabed, have been quantitatively analysed. These data are

supported by reinterpretation of historic acoustic datasets and review of the extensive literature published on the biology of the Rockall Trough. A new hierarchical deep-sea classification system has been developed and over 50 mapping units (biotopes - benthic assemblages plus surrounding habitat) defined. In addition a species image catalogue has been created and made available on line. Total coverage maps down to the substrate level of the classification have been produced and detailed biotope maps are being constructed for the surveyed areas. Predictive species distribution modelling is used to supplement assemblage level maps in the MPA scenario modelling process. The Hatton Bank map is presented as an example.

Age and growth of macrourid fishes from the Mid-Atlantic Ridge

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MAR-ECO and University of Glasgow

Diversity of life history traits was explored for 7 species of deepwater fishes of the family Macrouridae (*Coryphaenoides armatus*, *C. brevibarbis*, *C. carapinus*, *C. guentheri*, *C. mediterraneus*, *C. rupestris* and *M. berglax*), all inhabiting the mid-Atlantic Ridge of the North Atlantic. Biology of some of the species was studied previously in other waters, others were unstudied. Age was estimated for individual fish using otoliths sectioned along the transverse plane to expose assumed annual increments. The otoliths from all species presented increments resembling those accepted as annuli in other deepwater species for which validation experiments have been conducted. The age data were used to derive species-specific longevity, age distributions, growth curves, growth performance indices, and estimates of mortality.

Major differences in longevity and growth parameters were found between species, suggesting that the variation of life history strategies in deepwater fishes is extensive, even within the same family and general habitat. As expected, all species had relatively low growth rates. No trend of increasing longevity with depth of occurrence was found. Further, evidence is supplied for the presence of seasonality in the deep-sea which paves the way for more otolith-based studies on this family.

Organic matter turnover in the Arabian Sea oxygen minimum zone: the role of oxygen availability and benthic community structure

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The Arabian Sea Oxygen Minimum Zone is one of the largest deep-water bodies of persistently low oxygen, impinging upon 285,000 km² of continental margin sea floor. The ecology at the Pakistan and Arabian margins has been characterised by changes in benthic community structure along a depth-dependent oxygen gradient. However, the Indian continental margin has remained unexplored. Between September and November 2008 Prof Hiroshi Kitazato (JAMSTEC) led the first multi-national expedition to study the biology and biogeochemistry of the Indian continental margin. The aim was to investigate the interdependency between oxygen and organic matter availability, and benthic ecosystem structure and function across the Indian margin oxygen minimum zone.

In this presentation, both the megafaunal and macrofaunal assemblages and the role of the macrofauna in processing organic matter will be described. In situ pulse-chase experiments, using stable-isotope (^{13}C : ^{15}N) labelled organic matter, and visual survey of the megafauna were carried out along a down-slope oxygen gradient from a 530 m station within the OMZ core, at two parallel 800m stations and one 1100 m station in the lower OMZ boundary. Megafaunal surveys were also conducted at an additional 1100 m station and below the OMZ at 2000 m. Zonation was observed along the oxygen gradient both in the megafaunal and macrofaunal assemblages. With the exception of fish, metazoans were absent at the 530 m station. High megafaunal abundance was observed alongside peaks in macrofaunal abundance and biomass at the two 800 m stations. The highest uptake of labelled organic matter by macrofauna was observed at the 800 m stations, over a four day period. These results indicate that changes in ambient oxygen availability across the Indian continental margin control both benthic faunal assemblage structure and the role of the macrofaunal assemblage in processing organic matter.

The impact of deep-sea canyon conditions on meiobenthic structure and function

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For this study five deep-sea submarine canyon and one slope areas in the NE Atlantic were investigated within the framework of the EU FP6 HERMES project. Nematodes were used as a key group within the deep-sea meiobenthos. This study provides previously unavailable data on nematode structural and ecological diversity in canyon and referential slope sites, the intricate relationship between both, and their relation with local environmental conditions. The results suggest that community differences are mainly attributed to biogeochemical gradients along the vertical sediment profile rather than any other spatial scale. The link between trophic and structural diversity varied between different canyon ecosystems and suggests that the answer to the question “what maintains diversity in canyon ecosystems?” cannot be answered unilaterally. Enhanced hydrodynamic regimes characteristic for canyons have a profound influence on nematode structure and ecology, the link between trophic and structural diversity, and may – when attaining destructive proportions preclude the establishment of meiobenthic communities. The quality and quantity of the sedimentary organic matter dictates the characteristics of the nematode community, which seems to be adapted to the prevailing conditions. Interestingly, the hydrodynamic activity influenced the meiobenthic relation with available food: the more intense the disturbance, the tighter the relation between the nematode community and the quality and quantity of organic matter seemed to be.

Bathymetric patterns of meiofaunal standing stocks associated with the Kuril and Ryukyu trenches, Western North Pacific Ocean

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Abundance and biomass of metazoan meiofauna and their relationships with environmental factors [chloroplastic pigment equivalents (CPE), etc.] were studied quantitatively around the Kuril Trench (560–7090 m) and the Ryukyu Trench (1290–7150 m), which are located in eutrophic and oligotrophic regions, respectively. Faunal standing stocks and CPE amounts in sediments in the Kuril region were considerably higher than those in the Ryukyu region. In both regions, CPE tended to decrease with water depth and relatively high values were found in the deepest areas. Meiofaunal standing stocks, on the other hand, showed lower values than those expected from sediment CPE values at hadal stations. Our data suggest that the standing stocks of meiofauna in those trenches are controlled by the other factors other than the quantity of organic matter.

Beyond the Edge of the Sea; diversity of life in the deep ocean wilderness - A traveling exhibit merging the art with the science of the deep sea, featuring the illustration work of Karen Jacobsen, and the scientific expertise of Dr. Cindy Van Dover.

Jacobsen K. and Van Dover C.

In Situ Science Illustration
Duke University Marine Lab

BEYOND THE EDGE OF THE SEA is a traveling exhibition of watercolor illustrations by artist Karen Jacobsen, whose métier is deep-ocean landscapes and portraits of the exquisitely adapted animals that live in this unearthly world.

Artists have always sought and found inspiration in nature. But paintings of deep-sea animals and environments are very rare—they are as difficult to find as the deep-sea is to visit. Even now that thousands of individuals have dived in submersibles to the seafloor, only a handful have been artists. Only one is an artist who has visited the seafloor multiple times, in the Atlantic, the Pacific, the Gulf of Mexico, who has spent months at sea studying specimens recovered from deep-sea hot springs and cold seeps as they arrive fresh on deck, recording their colors and textures, their poise.

Jacobsen's deep-sea work fills many sketchbooks, hundreds of pages. It is a body of work that communicates concepts about the deep ocean using art as the lure, as a framework for exploring the natural history, as a medium with merit, as a means of communicating information about the world around us. The exhibit places emphasis on diversity of taxa, form, size, habitat, sources of energy. It also reminds us that, the ocean is an unexplored wilderness, a frontier for the next generation of explorers and researchers. People love ocean and space exploration, but the general public has little understanding of or appreciation for the complexity and diversity of deep-ocean ecosystems on Earth and the strange organisms that live in the deep sea, Beyond the Edge of the Sea challenges us to cherish the strange world of the abyss and reminds us that an entire ecosystem unimaginable just a few decades ago is a beautiful, living library for continued research.

Porifera (Sponges) of the deep Weddell Sea, Antarctic: preliminary results from the ANDEEP-SYSTCO expeditions, 2002–2008 with RV “Polarstern”

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Universidade Federal do Espírito Santo
University of Hawaii
Florida State University
University of Sao Paulo

During the ANDEEP-SYSTCO expeditions, sponges were sampled from the deep Weddell Sea and surrounding areas by various benthic sampling gears, especially Agassiz trawl, epibenthic sledge and Rauschert-dredge. Taxonomy and ecologic analysis was done, using several computer programs including MS excel and Past. So far, we identified more than 110 sponge species, of which at least 22 are new to science. They belong to the Porifera classes: Demospongiae, 77 spp. (12 new), Hexactinellida, 26 spp. (7 new) and Calcarea, 7 spp. (3 new). On the Antarctic shelf and slope, species of the circum Antarctic genus *Rossella* are dominant, whereas at Bathyal and abyssal depths they are replaced by *Bathydorus spinosus*, members of the family Euplectellidae and the genus *Caulophacus*. Contrary to the largely endemic shelf fauna, the Antarctic deep-sea Porifera comprise several cosmopolitan species, and show affinities to the deep Atlantic fauna. In the case of the rediscovered genus *Lonchiphora* sp. nov., collected at 2180 m in the Eastern Weddell Sea, the closest relative is a poorly documented species from the Pacific Sagami Bay. Many of the Cladorhizidae (carnivore sponges) are new to science and most of them new to the SO. The same is true the first bathyal and abyssal Calcarea discovered in the Antarctic Ocean (Rapp et al. submitted). Cluster-analysis of the sponges sampled during SYSTCO-expedition exhibit some distinct tendencies: The deepest station (5000 m) shows no species overlap with others, whereas the Stations between 500 and 3000 m show some similarities. The composition of the Antarctic sponge fauna changes successively with increasing depth, but keeps cohesive similarities down to ca. 3000 m. In the depth zone of about 4000–5000 m, a very distinct abyssal fauna is found. Despite the low sampling density, for most sponge taxa, our results point towards various zoogeographic links to other deep oceans.

Reconciling the link between deep-sea fish and surface water production: evidence from in situ observations.

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Deep-sea benthic communities primarily rely on an allochthonous food source. This may be in the form of phytodetritus or as food falls e.g. sinking carcasses of nekton or debris of marine macrophyte algae. Macrourids are one of the most abundant demersal fish in the deep-sea and are generally considered to be the apex predators/scavengers in these communities. Baited camera experiments and stable isotope analyses have demonstrated that animal carrion derived from the surface waters is an important component in the diets of macrourids; some macrourid stomachs also contained vegetable/plant material e.g. onion peels, oranges, algae. The latter observations led us to the question: is plant material an attractive food source for

deep-sea scavenging fish? We simulated a plant food fall using in situ benthic lander systems equipped with a baited time-lapse camera. Abyssal macrourids and cusk-eels were attracted to the bait, both feeding vigorously on the bait, and the majority of the bait was consumed in < 30 hours. These observations indicate: (1) plant material can produce an odour plume similar to that of animal carrion and attracts deep-sea fish, and (2) deep-sea fish readily eat plant material. This represents to our knowledge the first in situ documentation of deep-sea fish ingesting plant material and has since led us to question the importance of phytodetritus in deep-sea fish nutrition. Further in situ baited camera experiments simulating a pulse of phytodetritus at the seafloor revealed that macrourids were attracted to the bait within 8 minutes and fed vigorously on the bait consuming it in < 4 hours. These observations demonstrate that deep-sea fish may be able to utilise phytodetritus and in doing so short circuit the abyssal food web creating a direct connection to overlying surface water productivity.

Living fossils? New/old bone-eating snails from the deep-sea

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Deep-sea gastropods of the families Provannidae and Abysochrysidae (Abysochrysoidea) are common inhabitants of reducing environments including hydrothermal vents, cold seeps, sunken wood and whale-falls, where they graze on bacterial biofilms or host endosymbiotic bacteria. We report the discovery of a new abysochrysid genus and two species associated with whale-falls in Monterey Bay, CA. Gut content analyses revealed that the snails consume fragments of bone. In addition, 16s rRNA clone libraries from gills revealed the presence of bacteria that are genetically similar to thiotrophic endosymbionts associated with *Bathymodiolus* mussels. The new snails bear a remarkable resemblance to fossil shells associated with Cretaceous cold seeps. We hypothesize that their ability to inhabit a variety of reducing environments (sunken carcasses, cold seeps, etc.) has enabled abysochrysidoids to persist on very long evolutionary time-scales. To test this hypothesis, we conducted molecular phylogenetic analyses involving several mitochondrial, nuclear, and ribosomal gene loci. Known vicariance events and fossil evidence were used to calibrate a molecular clock that revealed the two species split approximately 40 mya. While it is uncertain how closely related the new genus is to the fossils, the living and fossil taxa are certainly representatives of the same lineage.

Temporal changes, during a fifteen-year period (1989-2004), in deep sea metazoan meiofaunal assemblages at the Porcupine Abyssal Plain, NE Atlantic

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Trends among major metazoan meiofaunal taxa were investigated based on 64 deployments of a multicorer at 13 time points over a period of fifteen years (1989 to 2004) at a site on the Porcupine Abyssal Plain (48° 50' N, 16° 30' W, 4850 m depth). This site is well known for strong seasonality in the deposition of organic matter to the seafloor and the massive increases since 1996 in the density of holothurian species, the so-called '*Amperima* event'. Total meiofaunal densities ranged from 884 to 3362 ind*25.5 cm² and showed a significant increase with time when time was represented by cruises, years and the '*Amperima* period' (1996–2004) vs. the pre-*Amperima* period (1989–1994). This pattern was driven mainly by the nematodes, which were the dominant taxon (~88% of total abundance). The third most abundant group, the polychaetes, also increased significantly in abundance over the time series, while the ostracods showed a significant decrease. Most other taxa, including the second-ranked group, the copepods (haracticoids and nauplii), did not show significant temporal changes in abundance. Ordination of taxon composition showed a shift from the pre-*Amperima* to the *Amperima* periods, a trend supported by the significant correlation between nMDSx-ordinate and time. The majority (52–75%) of the meiobenthic animals inhabited the top 2 cm of the sediment. There was a significant increase in the proportion of total meiobenthos, nematodes and copepods in the 0–1 cm layer, over the course of the time series. A downward movement deeper in the sediment was evident, in response probably both to the impoverishment and reworking of the surface layer and the downward mixing of organic matter in the sediment by larger macro- and megabenthic organisms.

Little-known large protists (Komokiacea and Xenophyophorea) in the macrobenthos of an abyssal polymetallic nodule field

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Komokiaceans, xenophyophores, and similar large (millimetre- to centimetre-sized) testate protists are often a dominant component of abyssal macrobenthic assemblages. Yet they are often overlooked or ignored, and as a result, few species have been described. Nevertheless, these foraminiferan-like organisms represent a major source of novel diversity in the deep sea, and their biogeography and biodiversity remain poorly documented. We studied the diversity and vertical distribution of komokiaceans and xenophyophores retrieved from sediment core samples collected from two areas in the Clarion-Clipperton polymetallic nodule field (sub-

equatorial NE Pacific), one located in the easternmost part of the field (sampled with a multicorer in 1997) and the other in its centre (sampled with a box corer in 2007). Amongst this often fragmentary material, we identified 11 morphospecies of xenophyophores and 85 komokiacean-like morphotypes, the highest level of alpha-diversity of the large protists ever reported in the deep sea. The komokiaceans included a large number of new species. Some could be assigned to known genera such as *Arbor*, *Baculella*, *Edgertonia*, *Lana* and *Reticulum*, while others represented new higher taxa. Fairly well-known species, such as *Septuma ocotillo*, *Ipoa fragila* and *Normanina conferta*, were also recognised. A large part of the xenophyophore species recognised are undescribed. These findings contribute to building baseline knowledge of abyssal communities in an area targeted for future commercial nodule mining operations.

This study was supported by the Polish Ministry of Science and Higher Education grant No. N N303v371036 and the Census of Marine Life CeDAMar project.

Population structure in the deep sea fish, roundnose grenadier (*Coryphaenoides rupestris*), as revealed by microsatellite DNA

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IMR
UIO

As an aid in revealing the importance of passive larval drift and active dispersal for population connectivity in deep water fishes, we applied statistical analyzes of microsatellite data in combination with oceanographic modeling and computer simulations. Roundnose grenadier (*C. rupestris*) were sampled (n=800) from throughout its geographic range in the North Atlantic and screened for microsatellite polymorphism at eight loci. Genetic differentiation among six sample locations and two temporal replicates identified a significant population structuring, and more markedly so than in most other deep sea fishes investigated to date. Amount of genetic differentiation was largely independent of geographic distance, and instead seems to be enhanced by bathymetric barriers in the form of shallow waters, and at least partly shaped by ocean current patterns. Biological and management implications of these findings are discussed.

Do organic contaminants accumulate more in submarine canyons than along the open slope? A case study of Blanes canyon, NW Mediterranean

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ICM, CISC
ICM, CSIC
IDAEA, CSIC

In recent years there has been increasing concern that the deep-sea might act as a global sink for contaminants that enter the marine environment. In particular, dense shelf water cascading (DSWC) events, which occur every 6–10 years in the NW Mediterranean Sea, could result in an enhanced transport of contaminants to the deep-sea. During these events, cold shelf water masses cascade down the continental slope transporting large amounts of sediment and organic matter to the deep-sea environment. As a significant portion of these water masses is channelled through submarine canyons, canyon environments might be subject to higher

contaminant input than the adjacent open slope areas. The present study aims at investigating the accumulation and potential effects of persistent organic pollutants (POPs) in deep-sea organisms from inside the Blanes canyon, NW Mediterranean, and the adjacent open slope combining chemical and biochemical (muscular and hepatic biomarkers) analyses. Species sampled include seven different deep-sea fish species (*Alepocephalus rostratus*, *Mora moro*, *Lepidion lepidion*, *Coelorynchus mediterraneus*, *Nezumia aequalis*, *Trachyrynchus scabrus* and *Bathypterois mediterraneus*) and two crustacean, *Aristeus antennatus* and *Geryon longipes*. We determined polychlorinated biphenyls (PCBs), dichlorodiphenyltrichloroethane and derivatives (DDTs), hexachlorocyclohexanes (HCHs), and polybrominated diphenyl ethers (PBDEs) levels in three deep-sea fish species collected inside and outside the Blanes submarine canyon at 1500m depth. Results indicate differences in contamination in one of the three species namely *Alepocephalus rostratus* with higher contaminant concentrations in individuals caught inside Blanes canyon. Potential effects resulting from contaminant exposure will be determined using biochemical analyses including cholinesterase (ChEs) and lactate dehydrogenase (LDH) activities in muscle tissue and hepatic biomarkers including Ethoxyresorufin-O-deethylase (EROD), catalase, carboxylesterase, Glutathione S-transferase (GST) activities. Variations in biological responses will be discussed in relation to environmental factors (i.e. contamination inside-outside canyon, depth) and their influence on biological processes will be examined (i.e. reproduction, growth).

Vertical distribution of chaetognaths in the Drake Passage

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Vertical distribution of the chaetognaths in the Drake Passage was studied in January 2010 between 600 S and 560 S. Biological data were supported by synchronous hydrological survey (temperature and salinity profiles, LADCP data) that made possible precise indication of the frontal zones and vertical distribution of the water masses. Material was collected at 6 deep stations crossing frontal zones. Chaetognaths were sampled from surface to a depth of 1000 m (once to 600 m and twice to 2000 m) with Juday nets (mouth area 0.1 m², mesh size 180 µm). Six species were recorded: *Sagitta gazellae*, *S. maxima*, *S. marri*, *Eukrohnia hamata*, *E. bathypelagica*, *E. bathyantartica*. Various species lived within different depth ranges except the dominating species *E. hamata* occurring at all sampled depths. Chaetognaths preferred upper layers, a total of 85 % of the individuals was samples within the layer 0–300 m. Patterns of the vertical distribution of various species are discussed along with their relation to different water masses. Influence of the frontal areas on the chaetognath distribution was analyzed with use of additional stations (depth ranges 0–300 m).

Undiscovered diversity of deep-sea serpulid polychaetes

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The Serpulidae are unusual polychaetes that are not restricted to soft sediments, but are sessile epifaunal suspension-feeders constructing calcareous tubes. Secretion of the tubes makes serpulids troublesome members of fouling communities and thus, best known serpulids are

commercially important fouling taxa from shallow-water locations. Serpulidae are also found in deep-sea environments and in the periphery of bathyal hydrothermal vent communities, however, their species diversity in the deep sea appears to be insignificant. Zibrowius (1977) listed 15 serpulid species and three decades later Paterson et al. (2009) had reported only 26 species from the depths greater than 2000 m world-wide. According to the most recent review by ten Hove & Kupriyanova (2009), the family comprises 346 nominal species, that is, the share of reported deep-sea species is 7.5%. Does this figure adequately reflect the situation with diversity of deep-sea serpulids? Here I bring to light unreported and thus, undiscovered diversity of deep-sea serpulid polychaetes hidden world-wide in research collections that remain unstudied with many species undescribed. The diversity of abyssal marine organisms remains poorly known not only because of obvious logistical difficulties with collecting, but also partly due to a lack of taxonomic efforts directed towards existing deep-sea collections.

Decreasing urea:methylamine ratios with depth in chondrichthyan fishes: a physiological depth limit?

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In marine osmoconformers, small organic osmolytes are accumulated inside tissues to maintain osmotic balance with seawater. Chondrichthyes use high levels of urea for this purpose. But due to urea's perturbing nature, stabilizing methylamines such as trimethylamine N-oxide (TMAO) and betaine are accumulated as osmolytes in cells for their counteracting properties, at about a 2:1 urea:methylamine ratio in shallow species. Moreover, a 2:1 urea:methylamine ratio has been found to be the most thermodynamically favorable mixture for protein stabilization. However previous work on deep-sea teleosts (15 species) and chondrichthyans (3 species) found an increase in muscle TMAO contents, along with a decrease in urea contents in chondrichthyans, with depth. We hypothesized that TMAO counteracts protein destabilization by hydrostatic pressure, which it does in vitro. To further test this pattern with many more species and depths, in this study we measured the levels of urea, TMAO, and betaine in white muscle of 13 species of chondrichthyans (holocephalans, sharks, rays, skates) caught at 100, 250, 500, 800, 1000, and 2000 m. At 100 m, muscles contained TMAO+betaine at 170 ± 50 and urea at 339 ± 39 mmol/kg wet mass (5 species). The urea:TMAO+betaine ratio was 2.1:1, correlating well with established values. Below 500 m, TMAO increased and urea decreased with depth; at 2000 m TMAO+betaine and urea contents were 283 ± 22 and 186 ± 5 mmol/kg respectively (2 species), with the urea:TMAO+betaine ratio declining to a significantly lower 0.66:1. This ratio declined exponentially with depth with a possible asymptote, suggesting a physiological limit to methylamine concentration. The possible role of such a limit in the approximate 3,000 m cutoff depth for occurrence of these fishes will be discussed. Support: National Science Foundation 0727135

Recovery of eukaryotic DNA from downcore deep-sea samples

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Previous studies revealed extremely high concentration of extracellular DNA down to 10 cm in deep-sea sediments. There are some evidences that DNA is preserved also in the deeper layers, but little is known about its origin and preservation. Knowing that the ancient DNA can last up to 100 kyr in cold settings, it is likely that the downcore deep-sea sediments would contain some amounts of preserved DNA. To test this hypothesis we attempted to amplify eukaryotic and specifically foraminiferal SSU rRNA gene fragments from total DNA extracts obtained from the surface down to 40 cm in the sediments collected during DIVA3 expedition to the South Atlantic. We observe a decrease of the amplification strength downcore, as expected for aDNA, with only fragments of about 100 bp recovered for the oldest samples. By selecting highly variable regions of the SSU rDNA we could successfully identify the eukaryotic taxa, which DNA was deposited in the sediments. We show that DNA could be preserved from total degradation possibly thanks to the anoxic, cold and very stable conditions that occurs at the deep-sea floor. Eukaryotic nuclear DNA recovery along geological time scales and associated sequence analysis might be highly relevant for the paleoceanographic reconstructions and evaluation of complex past environmental fluctuations as well as for phylogenetic calibration.

Pelagic zooplanktic trophic structure over the Charlie Gibbs fracture zone / subpolar front of the Mid-Atlantic ridge: a stable isotope and fatty acid analysis approach.

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Due to its remote location and rough terrain the MAR has been little studied up until recently. A current flurry of studies is investigating the fauna of the Mid-Atlantic ridge (MAR), a large longitudinally-extensive underwater feature of the Atlantic basin. Several studies in progress are investigating dietary relationships in disparate sections of the food-chain, with the ultimate aim to provide a full picture of the MAR food web. This study investigates the trophodynamics towards the base of the pelagic food web on either side of the subpolar front of the Mid-Atlantic Ridge. We compare stable isotope values of isotopes of carbon and nitrogen with fatty acid composition, in a range of macroplanktic species across a score of taxonomic orders (e.g. Euphausiacea, Decapoda, Amphipoda, Thecosomata) in order to investigate intra-and interspecies variation in trophic interactions. We investigated geographical variation in diet of species cosmopolitan to our research stations and those of previously published work on the MAR (*Sergestes arcticus*, *Themisto compressa*, *Meganctiphanes norvegica*, *Gnathophausia zoea*), and discuss the energy links between the epipelagic layers and the deep-water (2500 m on our stations on the MAR). Finally, in conjunction with data on the geographical and vertical variability in $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ of Particulate Organic Matter, we discuss the possible impact of differing primary production regimes (i.e low and substained to the South and intense and seasonal to the North) on plankton trophic interactions and thus for energy flow to the deep sea.

The Carbonate Nation: ecosystem engineering by carbonate-precipitating microbes at Costa Rica methane seeps

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Precipitation of authigenic carbonates by anaerobic methane oxidizing (AOM)/sulfate reducing microbial consortia is widespread at methane seeps. The resulting rocks and boulders provide hard substrate in an otherwise sedimented deep-sea environment. We examined the role of methane seep carbonates as habitat and their resident microbes as the base of the food chain at Mounds 11 and 12 on the Costa Rica margin at ~1000 m. Methane-oxidizing archaea (ANME) and sulfate-reducing bacteria comprised the majority of recovered 16S rRNA sequences from the interior of carbonates at sites of active seepage; microbial diversity increased in weathered, inactive carbonates. Animal densities were higher on 'active' rocks, with gastropods dominant. Polychaetes and ophiuroids were better represented at inactive sites. Rapid recolonization of experimentally placed carbonates suggests that the fauna is relatively opportunistic. The most common gastropods (*Provanna laevis* and *Pyropelta* spp.) appeared in large numbers at both active and inactive sites within 10 months, but colonizer densities and dominance were much higher at active sites. Gastropods (*Lepetodrilus* sp., *Cataegis* sp., *Pyropelta* sp.), *Kiwa* sp., and dorvilleid polychaetes were more common colonists at active sites whereas ophiuroids and polychaetes (hesionids, terebellids, lacydoniids, flabelligerids) dominated at inactive sites after 10 months. Stable C isotope signatures of carbonates and fauna reveal origins and diets, respectively. Inorganic $\delta^{13}\text{C}$ of carbonates ranged from +18‰ (dolomites) to -53‰ (methane-derived calcites). Carbonates were 0.7 to 3.4% organic C with Corg $\delta^{13}\text{C}$ values of -74‰ to -20‰. Light $\delta^{13}\text{C}$ tissue values suggest that lepetopsid limpets, chitons, provanids, nereidid and dorvilleid polychaetes incorporate methane-derived carbon, and in some cases archaeal lipids via grazing of AOM consortia. Other taxa incorporate carbon fixed by sulfide-oxidation. Through formation of authigenic carbonates, ANME consortia function as ecosystem engineers, providing attachment sites, refuge, and nutrition. The carbonate ecosystem offers functional similarities to vent, whale and wood substrates.

Frozen jelly in the blender: ubiquitous species, endemic species, and biodiversity in the gelatinous plankton community of Eastern Antarctica

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The gelatinous zooplankton community of Eastern Antarctica was investigated during Austral summer 2007–2008 (CEAMARC UmiTakaMaru 2008 Cruise) using a range of survey equipment, including a MultiNet, a Rectangular Midwater Trawl, a WP2 net, an in-situ autonomous High Definition Television Camera Recorder and an Autonomous Visual Plankton Recorder equipped with a colour digital camera. All groups, including the "impossible-to-preserve" ctenophores, were analyzed using fresh samples prior to preservation on board. Reference specimens were subsampled for molecular analyses and DNA barcoding data have identified gelatinous macroplankton exhibiting genetic exchange between communities in the Eastern Antarctic and in the North Pacific off Japan, as well as identifying putative cryptic species where Antarctic specimens differ from those in the North Pacific. Several species are undescribed and some were identified for the first time since their original description. Examination of still other species indicates that redescriptions will likely result in their being placed in different genera than those to which they are currently assigned. Community structure analyses were performed on the total dataset and one outcome was the separation of gelatinous plankton communities landward and further offshore from the continental shelf break. It is apparent that surveys of the deep water gelatinous community in Antarctic waters will yield many more surprises and that the use of modern technologies in such survey programs should be given high priority.

Diversity of Antarctic deep-water bivalves - with special references their macrobenthic assemblages in the Atlantic Sector of the Southern Ocean

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At present 158 species of bivalves are described for the Southern Ocean, of which 82 species occur in depths below 1000 m and 36 species are specific to the deep sea. Here we present data on the species richness, geographic and depths distributions of Antarctic deep-water bivalves as well as on the composition of their macrobenthic deep-water assemblages. Over the last ten years we collected abundance and composition data on deep-water bivalves by the means of an epibenthic sledge from the Atlantic sector of the Southern Ocean. More than 70 samples were taken during the expeditions EASIZ II (1998), ANDEEP I and II (2002), ANDEEP III (2005), BIOPEARL I (2008) and ANDEEP SYSTCO (2008) at depths from 160 to 6464 m. The sampling sites covered the South Atlantic from 65°W to 5°E and included the following areas: Falkland Trough, Shackleton Fracture Zone, Livingston Island, Deception Island, Elephant Island, NE Powell Basin, South Sandwich Islands, South Georgia, Shag

Rocks, Weddell Sea and Lazarev Sea. In this study we examine (1) the spatial distribution of species, (2) the extent of change of community composition between sites, (3) the relationship between species richness and environmental variables and (4) compare abundances patterns between sites.

Environmental assessment of the deep-water ecosystem to the west of the British Isles

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In recent decades, human activities have spread into deep-water ecosystems. Primarily fishing has developed in deep-waters but oil extraction is now also a component of human activities while other activities, such as mining for ore display significant perspectives for development into the deep waters. At the same time, land-based activities may impact deep-water ecosystems through e.g. acidification and spread of contaminants. Deep-water ecosystems are therefore impacted by a range of pressures induced by human activities. At the same time, deep-water ecosystems have generally a lower productivity than shallow water ecosystems, they include high biodiversity, vulnerable species and communities, while data and knowledge are more limited than for shelf and coastal ecosystems. The development of an ecosystem-based approach to the management of human activities is therefore particularly challenging in deep-water ecosystems. Here, ecosystem components and human pressures impacting them are analysed for the deep-water ecosystem (500–2000 m) to the West of the British Isles, a rather well studied deep-water area. The approach uses ecosystem characteristics and associated pressures and impacts as defined in the EU Marine Strategy Framework Directive (MSFD). An indicator-based piecewise assessment is then carried out for each ecosystem component. The results bring out the spatial scale and organization level for which the environmental status of the deep-water ecosystem can be determined using currently available information.

Proximate effects of the egg-eating bivalve *Acesta oophaga* on the morphology and reproduction of its siboglinid tubeworm host

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The limid bivalve *Acesta oophaga* surrounds the tube aperture of the cold-seep siboglinid polychaete *Lamellibrachia luymesii*, where it consumes the buoyant eggs of its host. Several morphometric and reproductive traits of the worms vary with the presence or absence of clams. Worm size, as measured by plume and vestimentum lengths, was higher when clams were present, but the length of distal segments, a likely correlate of tube growth, was reduced. Instantaneous fecundity (number of zygotes present in the ovisac) was an order of magnitude higher in worms with clams than without. It is not known whether this represents a true increase in egg production or a greater propensity to retain zygotes in the presence of an egg predator. Eggs removed from worms with bivalves were already fertilized, indicating that sperm bundles of these tubeworms must be dispersed through the water column rather than by direct contact of males and females, as has been suggested for another tubeworm species, *Ridgeia piscesae*.

Phylogenetic analysis of the vent shrimps and geographic distribution of the clades

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The families Alvinocarididae and Mirocarididae include 26 species and 8 genera of shrimps living at hot vents and cold seeps in the Atlantic, Indian, and Pacific oceans. Number of species and genera constantly grows, each year several species and a few genera being described. Now it seems to be reasonable to perform a phylogenetic analysis of all recently known species and to compare results with molecular and systematic data. A total of 20 available characters were analyzed, and phylogenetic trees were made with use of the programs Delta and Winclada. The characters of *Bresilia antipodarium* were used as those of an outgroup. The genera *Alvinocaris*, *Chorocaris*, *Rimicaris*, and *Mirocaris* are monophyletic. Recent genus *Opaepele* contains monophyletic branch (*O. loihi* and *O. vavilovi*) and *O. susannae* belonging to the branch *Mirocaris-Rimicaris-Chorocaris*. *Mirocaris* is positioned within the same branch, being, however, significantly different in morphological and molecular characteristics. In general, the data of the phylogenetic analyses made on the basis of morphological and molecular data are not contradicting. Species within the same clade do not occupy same geographic/ecologic areas; yet conversely, they are usually found in different oceans and habitats thus demonstrating parapatric speciation within the group.

Life cycle of *Rimicaris exoculata* above the North-Atlantic Ridge

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Extensive Russian collections of the dominant vent shrimp *Rimicaris exoculata* (5300 individuals) taken in 1994–2005 years during 34th–50th Cruises of R/V “Akademik Mstislav Keldysh” with the deep-sea manned submersibles “Mir-1” and “Mir-2” onboard were analyzed. These data made possible finding of the patterns of the spatial and temporal processes in the metapopulation of *R. exoculata* above the Mid-Atlantic Ridge. Material was collected from five vent fields: Rainbow, Broken Spur, TAG, Snake Pit, and Logachev. All studied populations of *R. exoculata* show remarkable size structure. Four stages characterized by fixed size patterns are usually present at all vent fields and in all seasons: (1) descending larvae with carapace length (CL 4–7 mm), recently settled juveniles (CL 8–11 mm), smaller non-breeding adults (CL 12–17 mm), and breeding adults (CL 18–23 mm). Population at Rainbow vent field shows a unique size structure. Reproductive analysis confirms existence of four stages revealed during morphological and size-structure analysis. Various stages demonstrate different patterns of distribution within vent field. They aggregate at preferred microhabitats and migrate from one to another while growing. These results along with other data give an evidence for duration of the life cycle of *Rimicaris*: 4 years. The plankton larvae grow in water column and settle (1st year), juveniles grow at a periphery of the vent fields and shimmering waters (2nd year), get mature and reproduce near black smokers (3rd and 4th years). Reproduction is synchronous and season-depending. Depending on various factors, similar population may occur at distant vent fields, while different black smokers of the same vent field may be settled with different populations. A model showing how colonization of the Mid-Atlantic vent fields occurs is proposed.

Extending our knowledge into the past: the rescue and reanalysis of historic zooplankton catch data from the Discovery investigations 1925–1951

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The earliest comprehensive plankton sampling programme in the Southern Ocean was undertaken during the early part of last century by the Discovery Investigations. These surveys were circumpolar in their distribution and totalled thousands of stations involving coordinated sampling that contributed enormously to our understanding, describing the Antarctic convergence and the critical role of krill in the food web. However, the synthesis of data used in the subsequent detailed ‘Discovery Reports’ attempted to answer important but very specific questions, and as such, not all the accumulated data was ever used. Furthermore, despite their significance, most of the original ecological data is not available to the scientific community. The BAS Discovery Project was set up to address this by recovering and extracting plankton net catch data from the original Discovery Collections, bringing together these highly valuable records into one single resource. As a result we are producing detailed circumpolar distributions of Southern Ocean planktonic species at 6 depth ranges, from the surface down to the deeper, colder waters of the mesopelagic zone, along with environmental and physical parameters that were recorded at each station. The standard protocol used in the Discovery Investigations of fishing from specific depths enables us to analyse both the vertical as well as horizontal distributions of zooplankton. Consequently these data are helping to fill gaps in the knowledge of, and the processes that govern the distribution of many important planktonic animals. It also allows for us to identify latitudinal shifts of species and changes in community structure by comparisons with modern accounts. Full exploitation of these data extends our time series into the past, enabling the use of new techniques for data exploration that were not available when originally collected. The presentation of this project will show what has been uncovered so far through our reanalysis of these unique and important data with specific emphasis on the mesopelagic zone.

A temporal analysis on the dynamics of deep-sea macrofauna: influence of environmental variability off Catalonia coasts (Western Mediterranean)

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A seasonal analysis of deep-sea infauna (macrobenthos) based on quantitative sampling was conducted over the Catalan Sea slope, within Besòs canyon (at ca. 550 m) and on its adjacent slope (at 800 m). Both sites were sampled in February, April, June–July and October 2007. Environmental factors influencing faunal distribution were also recorded in the sediment and sediment/water interface. Dynamics of macrobenthos at the two stations showed differences in biomass/abundance patterns and in their trophic structure. Biomass was higher inside Besòs canyon than on the adjacent slope at 800 m. The community is mostly dominated by opportunistic surface-deposit feeding polychaetes (such as Ampharetidae) and crustaceans (such as *Carangoliopsis spinulosa*) inside Besòs canyon, while subsurface deposit feeders (mainly the sipunculan *Onchmesoma steenstrupii*) were dominant over the adjacent slope. A

clearly different taxonomic composition was found on adjacent slope between infaunal and suprabenthic assemblages of polychaetes, the latter collected by a suprabenthic sledge. It was dominated by carnivorous forms (mainly *Harmothoe* sp.) and linked to higher near-bottom turbidity. Inside canyon a clear temporal succession of species in relation to food availability and quality and the proliferation of opportunistic species was consistent with higher variability in food sources (%TOC, C/N, C13) there compared to adjacent slope. This was caused by the influence of terrigenous inputs of river discharges. Spionidae and Flabelligeridae, in general considered as suspension-feeders, were more abundant in June–July coinciding with a clear signal of terrigenous C (depleted C13, high C/N) in sediments. By contrast, during October and under conditions of high water turbidity and increases of %TOM, opportunistic carnivorous polychaetes (Glyceridae, Onuphidae) increased. Total macrobenthos biomass found over Catalonian slopes, were higher than that found in the neighbouring Toulon canyon, probably because the two canyons are conditioned by different terrigenous sources, as the distinct connexion with river flows.

The devil is in the detail: ecological insight and management implications differ after modelling deep sea gorgonian distribution using different data resolutions

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In the northeast Atlantic, the UK Deep-Sea Marine Protected Area (MPA) Project was established almost 5 years ago with the aim of addressing where MPAs should be placed within the UK's deep-sea area. Part of that project involves the use of predictive species distribution modelling to 'fill the gap' in data coverage. Species distribution models offer a valuable contribution to today's marine environmental management and this is especially true in the deep sea where data are sparse and survey is expensive. However the resolution of available data is often poor and the consequences of this to modelling efforts are not clear. This study addresses the effect of the using environmental data at different resolutions on the performance of and ecological insight gained from predictive model outputs, using Hatton Bank as a case study.

Using gorgonian presence and absence records, in combination with environmental variables extracted / interpreted from acoustic data and video ground-truthing, Generalized Linear Models were constructed in order to predict gorgonian distribution across the Bank and to identify those variables significantly associated with it. Distribution records obtained from video transects were modelled against environmental data obtained from acoustic grids of three different resolutions; > 500 m, 200 m, and 25 m. Three models were constructed with different numbers of distribution records and combinations of environmental variables.

Substrate and depth were consistently and significantly associated with gorgonian distribution and included in the three final models. Geomorphology was also included in the final model for the 200 m resolution data. Model performance (based on the area under the ROC curve) differed significantly between the models with performance increasing with data resolution. High predictive accuracy is a prerequisite to the use of predictive model outputs to inform management and implications for management, in addition to ecological insight gained, is discussed.

A preliminary multi-parametric study on behavioural modulation in demersal decapods of Saanich Inlet by VENUS platform

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Dissolved oxygen is an environmental variable of ecological importance in marine ecosystems. Occurrences of hypoxia and anoxia are rapidly increasing in coastal and estuarine areas, most due to human activities. Understanding the effects of hypoxia on ecosystems is thus important for marine resource management. Saanich Inlet, British Columbia, is a highly productive fjord where anoxia is naturally present much of the year. There, instruments from the VENUS under-sea observatory allow a continuous monitoring of the seafloor. Between October and November we tested time-series photographic methods for studying biological rhythms of benthic organisms in Saanich Inlet, in relation with changes in environmental variables. Photos were taken with a remotely-controlled seafloor camera at hourly intervals at 3 different periods during October–December 2009. The manual counting of organisms was coupled with an automated counting method based on Scale-invariant feature transform image analysis algorithm implemented in matlab. Oxygen was low during the first days of the experiment ($<0.5 \text{ mg.l}^{-1}$). A first deep-water injection of oxygen produced an increase in ghost shrimp abundance. Subsequent oxygen intrusion events were associated with an increase in species diversity. In terms of activity rhythm, results suggested an overall significant response in shrimp behaviour to the local tidal regime in relation to changes in oxygen concentration. Macrofaunal community structure thus appeared to be determined by trade-offs between oxygen tolerance and biotic factors (e.g. food availability, predation). Our study shows that the use of permanent seafloor marine observatories can be effective for monitoring ecosystem changes due to hypoxia, a growing issue in the world's coastal oceans.

Food quality and season affect carbon cycling in deep sea sediments

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The supply of particulate organic matter to the deep sea is seasonal, consisting of highly labile, fresh phytoplankton and/or refractory detritus and zooplankton faecal pellets. Understanding the fate of the associated carbon in deep sea sediments is necessary to quantify their role in global biogeochemical cycles. Numerous studies have demonstrated that deep sea benthic communities respond rapidly to an influx of diatoms. However, little is known about how their response differs with season, or how it is influenced by organic matter 'quality'. Identical ^{13}C -labelling experiments were conducted in May and October to examine the hypotheses that a) food quality and b) season affect the rates and pathways of carbon cycling in a deep sea sediment community. ^{13}C -labelled diatoms or zooplankton faecal pellets, high- and low-quality food items respectively, were introduced to cores retrieved from 1100 m in

the Faeroe-Shetland Channel. Carbon mineralization and uptake of the labelled organic material into bacterial and macrofaunal biomass were quantified over 6-day incubation periods. The resulting data demonstrate that food quality and season both had significant effects on carbon mineralization rates but not on the quantities of carbon incorporated into organismal biomass.

Distribution and community structure of ultramicrobacteria in the Mediterranean Sea

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Miniature bacteria have been reported in the literature since 1974, and have often been associated with controversy and debate. Confusion over terms has done little to advance the field, but in recent years a consensus has been reached that defines ultramicrobacteria (UMB) as cells with a diameter of $< 0.3 \mu\text{m}$ and a volume of $< 0.1 \mu\text{m}^3$. Cells of this kind often approach the theoretical size limits proposed for cellular life and a number of reports have suggested that the majority of UMB cells represent the dormant or starvation forms of normal-sized bacteria. The presence of UMB in marine environments has been well documented but their significance has not been fully explored. Nevertheless, microfiltration of bacteria from aquatic samples using a $0.2 \mu\text{m}$ cut-off is common procedure in bacterial community structure studies, and bacterial abundance is typically enumerated by staining and counting cells concentrated on $0.2 \mu\text{m}$ filters. In the present study the term UMB is applied to bacteria collected on a $0.1 \mu\text{m}$ filter after passage through a $0.2 \mu\text{m}$ filter. This approach was used to fractionate bacterial communities in seawater samples collected from various depths in the eastern, central and western Mediterranean. Abundances were estimated by epifluorescence microscopy using Sybr-gold nucleic acid stain. UMB abundance was found to follow a distinct depth profile, unrelated to total cell count profiles. DGGE analysis of 16S rRNA genes was used to investigate the relatedness of ribotype communities present in the two size fractions. DGGE fingerprints of communities collected on $0.2 \mu\text{m}$ filters were found to be highly dissimilar from the UMB communities collected on $0.1 \mu\text{m}$ filters. Evidence from enrichment incubations further supports the hypothesis that the majority of UMB cells are not starvation forms as they did not increase in size in response to nutrient enrichments.

Habitat heterogeneity, biogenic disturbance, and resource availability work in concert to regulate biodiversity in deep submarine canyons

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Habitat heterogeneity is a major structuring agent of ecological assemblages promoting beta diversity and ultimately contributing to overall higher global diversity. The exact processes by which heterogeneity increases diversity are scale dependent and encompass variation in other well-known processes, e.g. productivity, disturbance, temperature. Thus, habitat heterogeneity likely triggers multiple and cascading diversity effects through ecological assemblages. Submarine canyons, a pervasive feature of the world's oceans, likely increase habitat heterogeneity at multiple spatial scales. However, our understanding of how processes regulating diversity, and the potential for cascading effects, within these important

topographic features, remains incomplete. Utilizing remote operated vehicles (ROV's) to take sediment cores, we were able to quantify faunal turnover in the deep-sea benthos at a rarely examined scale (1 m – 1 km). We document a remarkable degree of faunal turnover, and changes in overall community structure, at scales less than 100 m, and often less than 10 m, related to geographic features of a canyon complex. Ultimately, our findings indicate that multiple linked processes related to habitat heterogeneity, ecosystem engineering, and bottom-up dynamics are important to deep-sea biodiversity.

Collection and quantification of deep-sea macrobenthos: a case study of the polychaete *Melinnampharete gracilis*

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Collection and quantification of deep-sea macrobenthos is difficult, especially in locations with unknown substrate type. Thus, the selection of appropriate sampling gear is necessary considering the aims of the project. The ampharetid polychaete *Melinnampharete gracilis* has been found to be abundant and one of the dominant polychaete species in soft bottoms of the southern Gulf of California. Therefore, it constitutes a good example for the selection of the adequate gear used for the collection of deep-sea macrobenthos. Macrofauna inhabiting soft-bottoms of the Gulf of California was studied during seven oceanographic cruises, from 2000 to 2007. A total of 181 macrofaunal samples were collected between 360 and 2309 m depth with a benthic sledge (88 samples), a modified Karling dredge (77 samples), and a Reineck box core (16 samples) from which, *M. gracilis* showed a frequency of 10.23%, 7.79% and 6.25%, respectively. Abundance was estimated considering full and empty tubes. When more than 1000 tubes were found, the relationship between wet weight of subsamples and that of complete samples was also taken into account. Approximations of density were estimated considering the area covered by the Reineck box core (52.3 individuals/m²), the volume of sediment for the Karling dredge (0.1 to 7.5 individuals/m²), and the swept area with the average trawling speed, and the width of the benthic sledge (0.0003 to 4.05 individuals/m²). This study case allowed the determination of advantages and disadvantages of these methods based on frequency, density and size of organisms, and on their qualitative/quantitative character and their ability to collect sediment samples for other kind of analyses.

Influences of hotspots (canyon, coral reef, mud volcanoes) on macrobenthic communities in the deep Mediterranean Sea

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Due to its oligotrophy, deep-sea benthic communities of the Mediterranean Sea are generally depauperated. However, the seafloor of the Mediterranean Sea is heterogeneous, harbouring active canyons, coral mounds and cold seeps, which are generally associated with higher benthic biomass. The objective of this study was to test the consequences of contrasting trophic supplies on the alpha and beta diversity of macro-infaunal communities associated with different ecosystems. During the Envar and Medeco cruises, a box corer was used to

sample the macrofauna in the Var canyon (France), at the periphery of coral mounds on the Santa Maria di Leuca area (Italy) and in the vicinity of the Napoli (Crete) and Amsterdam (Turkey) mud volcanoes. The samples were sieved on a 0.25 mm mesh and sorted at different taxonomic levels. Macro-infaunal assemblages clearly differed between the studied “hotspots”, either in terms of densities, taxonomic richness and composition. These variations likely reflect, for a large part, different depths and trophic supplies along an east/west gradient in the Mediterranean Sea. Similar patterns were observed: the vicinity of the hotspots, such as the foot of the coral mound and the top of the mud volcanoes, is characterized by higher faunal densities and lower alpha diversity than away from them. While the taxonomic diversity of macro-infaunal communities seemed to decline in the vicinity of the so-called hotspots, the taxonomic composition also differed at relatively small spatial scales thus enhancing beta diversity and probably, the regional species pool as well.

A possible role for agglutinated foraminiferans in the development of deep-water coral mounds

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Exploration of deep-water bioherms dominated by the scleractinian corals *Lophelia pertusa* and *Enallopsammia profunda* along the east coast of Florida in ~400–800 m depth reveals an often dense and rich assemblage of small (~1–15 mm) epifauna on dead coral branches dominated by sediment-agglutinating astrophorid foraminiferans and accompanied by thecate and atehcate hydroids, sponges, stylasterids, anemones and barnacles. Three species of tree-like, agglutinated foraminiferans have been identified from coral substrates. The dominant agglutinating foraminiferan is an arborescent form up to 15 mm tall, similar to *Dendrophrya* T.S. Wright, consisting of a basal tube that gives rise to branchlets of successively decreasing diameter and thickly coated with fine-grained material including coccoliths and diatom frustules. Another species, identified as *Halyphysema* aff. *H. ramulosa* Bowerbank, constructs a cylindrical trunk of uniform diameter that successively bifurcates into smaller branches that terminate with clots of sponge spicules radiating from the open apertures. A third foraminiferan appears to be a more diminutive and highly-branched version of *Spiculidendron corallicum* Ruetzler & Richardson, a species that constructs its test from longitudinally-oriented sponge spicules. The large numbers of adherent foraminiferans generate an enormous adhesive, sediment-trapping surface area through the web of pseudopodia that hang suspended between the branches of their tree-like tests. This extensive sediment-trapping net may represent an important accelerated route for sediment deposition and bioherm growth relative to baffling of suspended sediment particles by the coral branches themselves. Although the foraminiferans and other epifauna appear to colonize recently dead (i.e., not yet discolored) coral branches, it is unknown if they contribute to coral mortality.

The ocean is not deep enough: pressure tolerances during early ontogeny of the blue mussel *Mytilus edulis*

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Early ontogenetic adaptations reflect the evolutionary history of a species. To understand the evolution of the deep-sea fauna and its adaptation to high pressure, it is important to know the effects of pressure on their shallow-water relatives. We analyse temperature and pressure tolerances of early life-history stages of the shallow-water species *Mytilus edulis*, phylogenetically closely related to Bathymodiolinae vent mussels. In *M. edulis*, successful fertilization under pressure is possible up to 50 MPa, at 10, 15 and 20°C. A slower embryonic development is observed with decreasing temperature and with increasing pressure; principally, pressure narrows the physiological tolerance window in different ontogenetic stages of *M. edulis*, and slows down metabolism. This study provides important clues on possible evolutionary pathways of hydrothermal vent and cold-seep bivalve species and their shallow-water relatives. Evolution and speciation patterns of species derive mostly from their ability to adapt to variable environmental conditions, within environmental constraints, which promote morphological and genetic variability, often differently for each life-history stage. Results support the view that a direct colonization of deep-water hydrothermal vent environments by a cold eurythermal shallow-water ancestor is indeed a possible scenario for the Mytilinae, challenging previous hypothesis of a wood/bone to seep/vent colonization pathway.

DNA-SIP analysis reveals rapid response of abyssal bacterial and crenarchaeal communities to phytodetritus deposition

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It is hypothesized that abyssal sea-floor matter cycling is dominated by the activity of prokaryotes, but little is known of their composition, responses to influx of particulate matter or relationships between diversity and ecosystem function, particularly mineralisation of organic carbon. The aim of this study was to determine the role of bacteria and crenarchaea in degradation of phytodetritus in a deep-sea site at 4,000 m water depth (Sta. M), 220 km west of the central California coast, with a long-term record of benthic C remineralisation rates. In situ measurement of rates and pathways of C degradation were combined molecular analysis, including DNA stable isotope probing (DNA-SIP). Stable isotope tracing experiments were carried out in situ with Oceanlab spreader systems using ¹³C-labelled phytodetritus. The relative abundance of bacteria and crenarchaeal phylotypes assimilating organic phytodetritus was determined in triplicate cores from enriched sediments using ¹³C labelled and unlabeled bacterial community DNA-DGGE. A limited number of bacterial species (1-3 OTUs) out of ~40 OTUs increased in relative abundance following enrichment, while several bacterial groups (1-6 OTUs) were negatively affected by the phytodetrital addition. Crenarchaea responded less than bacteria to phytodetrital enrichment, but there was evidence that they had a role in organic matter cycling under in situ conditions. Thus, deep-sea bacteria and crenarchaea have the potential to respond rapidly to organic matter pulses under in situ

conditions. Results also indicate high spatial heterogeneity of these microbial communities, since very different phyla responded to these pulse label carbon additions in replicate experiments.

Oxygen minimum seafloor ecological (mal) functioning

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Although organic matter (OM) settling on the seafloor is generally rapidly recycled, a key ecological process, large scale burial events manifests itself in the marine sedimentary record as organic carbon (Corg)-rich layers. Presently, this prevails under certain oceanic settings such as the oxygen minimum zones (OMZ) where OM accumulates in underlying sediments. A basic question that remains is to what extent does accumulation reflect a shunting of ecological processes: a niche unconquered? Experimenting with eastern Arabian Sea OMZ sediment we demonstrate that Corg accumulation here is not due to trophic satiation or low tolerance of biota to severe oxygen depletion but that sediment Corg has very low bioavailability that probably impairs biological transformation. In the first set of experiments, the impact of oxygenation on the benthic ecological functioning was examined by following the fate of ^{13}C -labelled diatoms in intact sediment cores incubated for 7 days under normoxic versus suboxic bottom water conditions. Tracer organic matter assimilation (by bacteria and fauna) and respiration was evident and similar under both treatments and demonstrates that the benthic community was not food saturated or hindered by severe oxygen depletion. In a second set of experiments, the bioavailability of in situ OMZ organic matter was determined directly through CO_2 production rates measurements in bottle sediment-water slurry incubations. In contrast to fresh tracer algal carbon which had a half-life 0.07 years, OMZ surficial sediment OM half-life was ~ 67 years already in very early diagenesis. However, although evidently excluded from immediate first-hand biotic transformation, this represents a niche on its own: a rapid shift from the “fast (biological)” to the “slow (geological)” carbon cycle along the continuum of OM recycling. Furthermore, in the a third set of experiments; we compared OM bioavailability in sediments with contrasting geochemical characteristics, including an ancient Corg-deposit. These results suggest that while this rapid shift may be common or characteristic of large scale accumulation events, the trigger mechanisms may not be uniform.

Distribution and abundance of deep-sea corals upon an Axial Volcanic Ridge (AVR) of the Mid-Atlantic Ridge at approximately 45° W 30' N

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The deep-sea floor below 3,000 m occupies 50% of the surface of the planet. Much of this seafloor is composed of fine sediments and most studies of faunal composition to date have concentrated on soft substrata. Little is known about rocky areas with the exception of rock-hosted deep-sea hydrothermal vents. This study uses video footage from the submersible Isis taken during a cruise to the Axial Volcanic Ridge (AVR) of the Mid-Atlantic Ridge at approx 45°30' N to assess the coral distribution and abundance within the area. Abundances per 100 m are calculated and mapped using ARC GIS. The data are separated into four substratum types, sediment, sloped rock flat rock and mixed rock and sediment, with both abundance and community being compared.

Sedimented and rocky areas supported different corals, with sediment having a higher occurrence of pennatulids than rock. Sloped rock was found to have the highest abundance of corals present. It is suspected that this increase in abundance reflects a firm base for attachment of the corals and a higher food availability resulting from enhanced current flow on sloping topography.

Biomass relations in the Faeroe-Shetland Channel: an Arctic-Atlantic boundary environment

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Community standing stock is expected to decrease with depth in the deep sea. However, in the Faroe-Shetland Channel this does not appear to always hold true, with abundance and biomass exhibiting different patterns with depth dependent on the size of mesh used to collect the fauna. Macrofauna were collected using a Day grab, box corer and Megacorer dependent on the sediment type encountered. A number of stations were sampled at depths ranging from ~150 m to ~2000 m in the Faroe-Shetland Channel region. Samples were routinely sieved on 0.5 mm mesh sieves, with samples collected from a detailed bathymetric transect West of Shetland transect also collected on a 0.25 mm sieve. In the smaller size fraction (>0.25 <0.5 mm) macrofaunal abundance showed a classic decline with depth, whilst the larger (>0.5 mm) fraction tended to show an increase to ~800 m before decreasing. Macrofaunal biomass, however, exhibited a different pattern, with both fractions showing an increase in biomass to ~500 m before decreasing. Dominant phyla were further examined in further detail. Unsurprisingly, polychaetes dominated the standing stock accounting for more than 60% of total abundance (~50% in the smaller size fraction; ~70% in the larger size fraction) and more than 35% of total biomass (~50% in the smaller size fraction; ~35% in the larger size fraction). As found in our previous studies of diversity, water temperature appears to be the key parameter influencing standing stocks in the Faroe-Shetland Channel. However, sediment organic matter content correlates reasonably well with the abundance of the larger size fraction. It is possible that peaks in faunal abundance between 550 m and 700 m on the West of Shetland transect may correspond to enrichments of labile organic matter at these intermediate depths.

Utilization of dissolved organic matter by the deep-sea benthic community at the Sagami Bay, Japan

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Consumption process of dissolved organic matter and particulate organic matter in the deep-sea benthic ecosystem were evaluated by conducting in situ tracer experiments at the central part of Sagami Bay, Japan (water depth 1453 m). Both ^{13}C -labeled glucose (an example of labile dissolved organic matter) and *Chlorella* (an example of fresh algal materials) were injected into a series of in situ incubation cores and were incubated for 1, 2, and 9 days. Incorporation of both carbon sources to benthic foraminifera and metazoans were examined based on enrichment in ^{13}C of their soft tissues. Incorporation to archaeal biomass were also evaluated by examining the ^{13}C -labeled lipid biomarker abundances during the incubation. *Chlorella* was incorporated by some foraminiferal species with various extents ranging from 0.0 to 40% of their cell. On the other hand, glucose was incorporated into every examined species with similar extents ranging from 0.1 to 0.3% of their cell. Many foraminiferal species incorporated glucose faster than *Chlorella*. Results indicate that dissolved organic carbon in the sediments may provide an accessible food source for many benthic foraminifera while rate and extent of phytodetritus utilizations substantially differ between species. Incorporations of glucose by archaea were lower than those of foraminifera, suggesting that their metabolic activities are relatively low at the deep-sea floor. After 9 days of in situ incubation, 26.4%, 1.7%, 0.1%, and 3.8% of added *Chlorella* was detected in the bulk sediment, foraminiferal biomass, metazoan meiofaunal biomass, and in the respired CO_2 , respectively. Those of glucose were 5.3%, 0.04%, 0.00%, and 4.6%, respectively. Nearly half of the recovered ^{13}C in glucose cores were found as respired CO_2 , while those of *Chlorella* were found mainly as sedimentary organic matters. Labile dissolved organic matter may serve an accessible food sources for certain benthic organisms, and quickly mineralized at the deep-sea floor.

Biogeographic analyses of deep-sea fauna using species habitat models

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The large-scale spatial distribution of seafloor fauna is still poorly understood. Biogeographical syntheses have been impeded by spatially heterogeneous collection effort and the high cost of sampling oceanic habitats. One solution is to 1) model species potential distributions, using environmental predictors to infer species ranges from known occurrences, and then 2) derive biogeographic patterns using multivariate statistical techniques on the modelled species data. This method was used to analyse a large (>46,000 records) dataset of ophiuroid (brittle-star) distributional data from the southern hemisphere using a variety of presence-only modelling and multivariate techniques. The advantages and pitfalls of these techniques will be discussed.

Pressure tolerance of the shallow-water caridean shrimp, *Palaemonetes varians*, across its thermal tolerance window

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To date there is no study available that has assessed the full physiological scope of a marine invertebrate species with respect to both temperature and hydrostatic pressure. Adult specimens of the shallow-water shrimp species, *Palaemonetes varians*, were subjected to a temperature/pressure regime from 5 to 30°C and from 0.1 to 30 MPa. Rates of oxygen consumption and behaviour in response to varying temperature/pressure combinations were assessed. Rates of oxygen consumption were primarily affected by temperature. Low rates of oxygen consumption were observed at 5 and 10°C across all pressures and were not statistically distinct ($P = 0.477$). From 10 to 30°C, rates of oxygen consumption increased with temperature; this increase was statistically significant ($P = < 0.001$). *P. varians* showed an increasing sensitivity to pressure with decreasing temperature; at all temperatures, shrimps were capable of tolerating hydrostatic pressures found outside their normal bathymetric distribution. Loss of equilibrium (LOE) in > 50 % of individuals was observed at 11 MPa at 5°C, 15 MPa at 10°C, 20 MPa at 20°C, and 21 MPa at 30°C. The physiological capabilities of *P. varians* to tolerate a wide range of temperatures and significant hydrostatic pressure are discussed in the context of the monophyletic relationship between shallow-water palaemonid and deep-sea bresiliid shrimps; and the likelihood of shallow water species to undergo bathymetric range shifts in response to warming of surface waters in the course of global climate change.

Insights into the evolution and biogeography of chrysogorgiid corals

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As currently described, the octocoral family Chrysogorgiidae is found in all oceans and at all latitudes, between 10 and 4492 m depth (although $>75\%$ of species are below 200 m). Chrysogorgiids are also characterized by strong taxonomic asymmetry: while 12 of 13 genera comprise less than 10 species, one (*Chrysogorgia*) is one of the most speciose alcyonacean (soft corals and gorgonians) genera. These characteristics (distribution and taxonomy) make chrysogorgiids noteworthy as a model system to study radiation and diversification in the deep-sea. To better understand the evolution and biogeography of this group, we inferred phylogenetic relationships based on taxa from 11 genera, using both nuclear (18S) and mitochondrial (cox1 and msh1) markers. Genetic data were compared to geographic and bathymetric distributions, based on our collections, museum records, and a literature review. All shallow-water genera, and two of eight deep-water genera, appear more closely related to other octocoral families than to the remaining deep-water chrysogorgiid genera (including *Chrysogorgia*), which form a monophyletic clade. This clade is sister to gold corals (Primnoidae) and bamboo corals (Isididae), families which also have diversity peaks in the deep sea. This suggests that the monophyletic deep-sea chrysogorgiids diversified in the deep sea. Nevertheless, several species of *Chrysogorgia* were described from depths shallower than

200 m, and msh1 haplotypes were found from specimens sampled as shallow as 150 m, suggesting the emergence of some *Chrysogorgia* species. Contrary to our expectations, shallow occurrences of *Chrysogorgia* were not polar. The biogeography of *Chrysogorgia* is further detailed in a poster presented at the 12th DSBS.

Meiofaunal biodiversity and ecosystem functioning at the Galicia Bank (NE-Atlantic)

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Seamounts are unique ecosystems as they are (1) traditionally considered as hot spots of biodiversity because they often display a high endemism and species diversity, and (2) characterized by enhanced near-bottom currents. However, they remain highly under-investigated. In June 2008, the Galicia Bank in the NE Atlantic, offshore the coast of NW Spain, was sampled at 120 m, 1900 m and 3000 m water depth. From March till August, the deep nutrient-rich waters surrounding this seamount are subjected to upwelling, leading to an increased productivity in surface waters. The Galicia Bank has been characterized geologically, but biological information appears rather scarce. This is the first time the meiofaunal (nematode) community structure is studied in detail (in terms of densities, biomass, and diversity of taxa, genera and species) along a bathymetrical gradient at the Galicia Bank. Moreover, the linkage between biodiversity and ecosystem functioning, of which the latter is inferred by their feeding behavior, is examined.

This research is performed within the framework of the ESF-funded BIOFUN project which main aim is to characterize, under an ecosystem-approach, slope and abyssal habitats, from viruses to megafauna, to understand linkages between biodiversity and ecosystem functioning in 4 sites of contrasting environmental conditions (i.e. Galicia Bank, Western Med, Central Med and Eastern Med).

Temporal variability in polychaete assemblages of the abyssal NE Atlantic Ocean: the species response

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Temporal variability in the species composition of the deep-sea polychaete fauna on the Porcupine Abyssal Plain, NE Atlantic Ocean was assessed over a 9-year period. Samples were studied from 8 cruises between August 1989 and September 1998. The fauna were dominated by species of the families Cirratulidae, Spionidae and Paraonidae. Six species from the Cirratulidae and Spionidae showed significant increases in abundance coinciding with large-scale changes in benthic megafauna. The abundance of individual polychaete species changed by a factor of two to three. Not all polychaete species responded in the same way and at the same time. The changes in species was for the most part from existing elements of the fauna and were not new immigrants. Despite the obvious response at the family and higher

taxon level the changes in abundance observed for key species was often not significant. The reasons for this discrepancy will be discussed. This study illustrates the importance of assessing faunal responses to environmental change at the lowest taxonomic level possible.

Multigene analysis of polymorphism versus divergence reveals allopatric speciation processes and demographical expansion along the East Pacific Rise

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Demographic history and past gene flow between populations of deep-sea hydrothermal vent species along the East Pacific Rise (EPR) were assessed using a phylogeographic approach combining a classical allele-frequency-based analysis and more sophisticated coalescence-based methods. A comparative phylogeographic COI-based analysis of seven species (one bivalve, three gastropods, three polychaetes) showed the occurrence of a vicariant event associated with the raise of a physical barrier between the Northern and Southern EPR, 1.3 Mya probably due to the formation of transform faults in the equatorial region (0° - 7°25'S). This fauna separation was then followed by a more recent (< 0.5 Myr) population expansion in the South for all species. The use of a multilocus approach (three nuclear genes for each of three targeted species) confirmed the vicariant and expansion hypotheses and suggested that the barrier is semi-permeable for all tested taxa leading to more or less extended secondary contact zones across the equator. This analysis confirmed the preponderant role of allopatric speciation in shaping the hydrothermal vent biodiversity.

Biodiversity, trophic linkages and carbon flow in the deep-sea benthic food-web

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We aim to elucidate trophic linkages from microbes to metazoans in deep-sea sediments using multiple approaches (lipid and biomarker analysis, stable isotope tracers). During different cruises we have collected an elaborate set of deep-sea sediment samples (1900 m) to be subject to a wide diversity of analysis (biomass and composition of benthic community, lipid and stable isotope analysis) and we performed onboard-ship manipulative laboratory experiments. The basic approach also involved adding a tracer amount of potential food to cores (isotope labeled POM and DOM obtained from algal material -*Thalassiosyra pseudonana*-), the fate of which could be followed in the different components of the seafloor community. Further insight into the dynamics was addressed by varying the O₂ concentration in the overlying water of the cores. Detailed analysis of the response of each component (bacteria versus metazoans) provides new insights into the relationship between seafloor community structure and basic seafloor functioning.

Phylogenetic diversity of octocorals in the Gulf of Mexico

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Octocorals (Anthozoa: Octocorallia) create extensive habitat heterogeneity in the deep-sea (> 200 m) worldwide. In the Gulf of Mexico (GoM), octocorals are common and diverse and inhabit depths up to 3000 m. Octocorals have been historically well documented in the GoM, but recent cruises to deepwater habitats in the region yielded additional distribution data, including species previously unreported. Currently, data are lacking on the phylogenetic diversity and assemblage structure of octocorals throughout the GoM. We set out to test the hypothesis that similar habitat types in different areas of the GoM will contain octocoral assemblages with similar phylogenetic community structure. We are also investigating the population connectivity in a few common species [*Callogorgia* spp. (Primnoidae)] of gorgonians. In 2008 and 2009, remotely operated vehicles were used to sample corals from 16 sites across the GoM at depths ranging from 200-2500 m. Approximately 40 octocoral taxa represented by 175 individuals were collected, including 76 specimens of *Callogorgia* spp. The mitochondrial MSH gene, unique to Octocorallia, and ND2 gene were amplified and sequenced. High phylogenetic diversity was found at depths > 800 m and also at the easternmost site, the West FL Slope (400 – 450 m). The octocoral assemblage at the West Florida Slope was distinct from the other GoM sites, possibly due to the Loop Current regime. At a few sites, at least two different *Callogorgia* spp. formed extensive monotypic stands. In addition, we extended the geographical range of a recently described species, *Sibogorgia cauliflora* Herrera et al. 2010, to the GoM. Determining the pathways and degree of genetic exchange among GoM gorgonians will be important to effectively conserve deepwater coral habitat in the region.

Life under glass houses: the impact of glass sponges on meiofaunal abundance in sediments at abyssal depth in the NE Pacific

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One of the long-standing hypotheses for the maintenance of high species diversity in deep-sea sediments is habitat heterogeneity provided by biogenic structures. In this study, we assessed the impact of hexactinellid (glass) sponges (specifically, in the genus *Hyalonema*), on the abundance and gross taxonomic composition of meiofauna in deep-sea sediments. We used the submersible “Alvin” to carefully collect sediment cores adjacent to glass sponges at ~4000 m depth at Station M in the NE Pacific. Each core was paired with an additional core of ambient sediments taken ~2 m away, outside of the likely influence of the biogenic structure. We also determined sediment contents of phytopigments (chlorophyll a and phaeopigments) in the two sets of cores. Surprisingly, our results do not indicate any significant differences between the “near” and “away” cores in the abundances of higher-level taxonomic groups of meiofauna. Similarly, no significant differences were found between pigment concentrations in the “near” and “away” cores, although a tendency towards higher chlorophyll a contents in

the uppermost sediment layer and a sharper drop below it was observed in the “near” cores compared to those taken away from the sponges. Deep-sea sponges, which themselves may harbour diverse assemblages of fauna (e.g., attached to sponge stalks), have received increasing attention from government and non-governmental organizations in recent years due to the potential loss of habitat and associated biodiversity with bottom trawling in deeper waters beyond the continental shelf. Our study is specific to one type of sponge at one depth, and our results do not preclude the importance of other types of sponges and at other depths in impacting biodiversity in sediments.

This study was supported by the Mary Sears Visitor Program Award of the Woods Hole Oceanographic Institution.

Spatial variability in size-related shifts in deep-sea fish trophodynamics elucidated by stable isotopes

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Demersal fish play an important role in the deep-sea ecosystem by acting as a link to mobile food in the water column or by breaking down large food parcels. Both these processes allow food to be dispersed over larger areas and made available to other deep-sea fauna. However, it is difficult to elucidate diet, dominant energy sources or shifts in diet with size from gut content analysis or baited video experiments. To investigate the trophic role of deep-sea fish, and whether this changes with size, four species of deep-sea fish (*Antimora rostrata*, *Coryphaenoides armatus*, *Coryphaenoides brevibarbis* and *Halosaurus macrochir*) were collected from the Mid-Atlantic Ridge at 3 stations, 2700m deep, north and south of the Charlie Gibbs Fracture Zone in 2007 and 2009. Stable isotopes of carbon and nitrogen were used to examine size related shifts in diet and whether these relationships varied spatially or between years. $\delta^{15}\text{N}$ increased with size in *A. rostrata*, *H. macrochir* and *C. brevibarbis* at all stations where as in *C. armatus* these relationships were not consistent. Weak positive and negative trends were observed in $\delta^{15}\text{N}$ with size for *C. armatus* north and south of the CGFZ, respectively. $\delta^{13}\text{C}$ consistently increased with size in *A. rostrata* but the relationships varied spatially in the other species. There was a dramatic shift in $\delta^{13}\text{C}$ from -15.6‰ to -18.9‰ in *C. armatus*, indicative of a switch from benthic to pelagic food sources, at the southern station but a weak positive shift at the northern stations. *Coryphaenoides brevibarbis* exhibited weak negative $\delta^{13}\text{C}$ size-based trends in 2007 at the northern station but these were reversed in 2009. The results suggest that some species of deep-sea fish have a higher degree of feeding plasticity than others and may vary their foraging behaviour or diet depending on prey availability.

Plans to protect deep-water coral ecosystems along the European margins: new insights from phylogenetic analyses of the associated Porifera

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Large-scale phylogenetic analyses have proved very useful for establishing baselines of species diversity and the management of marine resources. They are essential to explain the origin and evolution of marine biodiversity. Knowledge of species boundaries, distribution and processes that control species ranges is mostly limited to popular shallow-water coral reefs. However, less attention has been paid to deep-water coral and sponge ecosystems, despite the fact that they thrive along the European margins.

Within the present study, we used the mitochondrial (COI) and nuclear gene fragments (28S rDNA and the ATPS intron) in a comparative phylogenetic/phylogeographic study of widely distributed sponge species in order to test the hypothesis of different lineages of cold-water coral associates along our European coasts. The molecular diversity within *Hexadella* species (Porifera, Verongida, Ianthellidae) and *Plocamionida* (Porifera, Poecilosclerida, Hymedesmiidae) retrieved from the European shallow-water environment to the deep-sea coral ecosystems was assessed in order to get insights into (i) the genetic variation of these species within, between and outside reefs (ii) the connectivity or isolation of these reefs along the European margins.

Signatures of both genetic differentiation as well as gene flow across large areas in the deep-sea sponge species stress the need to protect multiple lineages of cold-water coral reefs along the European margins. Indeed deeply divergent clades congruent across the mitochondrial and nuclear gene fragments suggest the occurrence of several cryptic species, while widely distributed specimens within these clades suggest an old or putative recent connection between the reefs. Once revealed by molecular markers, an ‘a posteriori’ search of diagnostic phenotypic characters and description of these new cryptic species is the next step for taxonomists.

Composition and spatial patterns of cold seep communities from different geological structures in the deep Eastern Mediterranean Sea

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The structure of faunal assemblages associated with cold seep ecosystems were investigated in contrasting geological settings of the Marmara Sea, Mediterranean Ridge and Nile deep sea fan. In each of these regions, distinct microhabitats were identified by the presence of visually dominant species and differences in the nature of the substratum. These include reduced and bioturbated sediments, sediments with bivalve shells and carbonate crusts. Tube cores and grab samples were used to estimate mega- and macro-faunal community structures in terms of composition, density, diversity and biomass. Geochemical conditions were measured in situ at

the sediment-water interface and within the sediment in the microhabitats. Relationships between the repartition of the fauna and environmental conditions were investigated. Moreover, community structure and links between faunal distribution and abiotic factors were compared at different spatial scales (local, regional). The results show that overall the Napoli mud volcano is the richest geological structure in terms of numbers of taxa while the Nile deep-sea fan sites are the poorest and would probably benefit from additional sampling. Within all sites, a high heterogeneity in faunal composition was observed both among the different microhabitats, as well as within each microhabitat. Our data suggest that gradients of methane and oxygen concentrations and the nature of the substratum were the main structuring factors explaining the distribution of the fauna at each site. In the light of our results, local microhabitat characteristics appear to strongly influence the structure of benthic communities associated with Mediterranean cold seeps.

Looking at some chemosynthetic species: from Atlantic to Eastern Mediterranean

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Bathymodiolin mussels, lucinids and thyasirids are among dominant members of vent, seep, and organic-fall communities worldwide. During last years the discovery of the same (or sister) species on both sides of the Atlantic reinforced the Atlantic Equatorial Belt' hypothesis. This hypothesis postulates recent exchanges between these geographically distant populations. If studying the hosts is crucial to understand their evolution, the study of their associated bacteria is also essential to understand the evolution of "symbiotic systems" and their level of adaptability. Molecular analyses of bivalves from 3 sites (Gulf of Guinea (GoGui), of Cadiz (GoC) and eastern Mediterranean (East Med)) are compared and discussed. The discovery of two trans-Atlantic species in the GoC (*Bathymodiolus mauritanicus* - "B." *childressi* complex and *Idas* sp – sister species of *Idas macdonaldi*) highlights the GoC as a potential connexion point between Atlantic and Mediterranean. Additionally the occurrence of both species at the same mud volcano allows us to discuss if or not associated bacteria are clustered geographically or according to similarity of host species. The high number of bacterial phylotypes present in *Idas* sp. Med (6 against 1 in the GoC) could be an evolutionary adaptation to the local environment since they are sister species with *Idas* (GoC), and while the former occurs on several substrates (e.g. carbonate crusts, wood), the latter species were only found in wood-filled colonization devices. Symbioses in deep-sea lucinid and thyasirid are poorly known, despite their occurrence and abundance in these environments. Three different thyasirids species from the three sites were studied here and their symbiont phylogeny appeared to be complex and intriguing, as is host phylogeny. Data presented here will help to understand the links between organisms from all these different areas, and infer about their dispersion and evolution, not only as species but also as host, and their symbioses.

Protection of deep-sea ecosystems by Regional Fisheries Management Organisations (RFMOs)

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UN General Assembly Resolutions 61/105 and 64/72 called for protection of vulnerable marine ecosystems from significant adverse impacts arising from bottom fishing and to sustainably manage fish stocks in the deep waters of the high seas. Key requirements of the UN Resolutions include: (i) Conduct assessments of whether bottom fishing activities have significant adverse impacts on vulnerable marine ecosystems (VMEs). (ii) To ensure that if fishing activities have significant adverse impacts that they are managed to prevent such impacts or not authorized to proceed. (iii) To establish and implement protocols to cease fishing where an encounter with vulnerable marine ecosystems occurs during fishing activities and to report such encounters so that appropriate measures can be adopted with respect to that site. (iv) To implement measures in accordance with the precautionary approach, ecosystems approaches and international law and to sustainably manage fish stocks. RFMOs that manage deep-sea bottom fisheries were assessed with respect to implementation of the UN Resolutions. It was found that only some RFMOs have undertaken assessments of the impacts of deep-sea bottom fisheries on VMEs. Some RFMOs have established areas where bottom fisheries are not permitted to protect known VMEs. However, in many cases, no such areas had been established or proposed. Encounter protocols have been widely adopted but in many cases they were not based on appraisal of what species may comprise VMEs within regions and likely encounter rates that signified a VME encounter. In almost all cases, sustainable management of deep-sea fish stocks, including target and by-catch species, was not possible because of a lack of data. Even where scientific recommendations are made these were often exceeded by quotas set by RFMOs. Recommendations are made for improvement of management of high seas deep-sea fisheries.

Satellite to seafloor: ocean colour and holothurian distribution

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Large-scale biogeographic patterns in the deep sea remain poorly understood. Small-scale studies are hampered by the patchiness of the benthic environment resulting in conflicting ecological interpretations. This patchiness fades at larger scales, so that global scale studies of species distributions and key environmental factors will improve our understanding of deep-sea biogeography. A database of global distribution records for 273 species (32 genera) of deep-sea holothurians was compiled. These records will be GIS-mapped and analysed with various environmental factors including bathymetry, primary production, seasonal variation in primary production, organic matter flux to the seafloor, bottom water temperature and bottom current regime in order to examine the controls on faunal distributions. For example, are distributions more affected by the magnitude or the seasonality of surface water primary production? Do oligotrophic areas form barriers to the dispersal of deposit-feeding benthos? Do species with larger egg sizes have greater geographic ranges? Are there topographic or hydrographic barriers to the dispersal of deep-sea holothurians? In addition, a

phylogeographic analysis of a number of deep-sea holothurian species thought to have cosmopolitan distributions will be undertaken. Sequencing of the mitochondrial Cytochrome Oxidase 1 and the ribosomal 16S genes will be used to investigate intra-specific genetic structuring and the possible effect of environmental controls on within-species genetic population structure.

A synthesis of seamount ecological paradigms: fact, fiction and the future

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Seamount ecology has a relatively short history, but nonetheless a number of ecological paradigms have seemingly become cemented in the scientific literature and in the minds of advocates for seamount protection. These paradigms have contributed to the concept that seamounts are special or unique habitats, the faunal communities of which are sufficiently different from, and/or more fragile than, those of other deep-sea habitats as to warrant particular scientific attention and are of exceptional ecological worth. This concept, plus knowledge of the threat posed by fishing to seamount habitat and communities, has stimulated a number of seamount-focused research projects in recent years. Here we evaluate the evolution of paradigms in seamount ecology, consider the robustness of these paradigms with reference to recent research findings, identify emerging paradigms, and suggest future ecological research directions involving seamounts in a wider deep-sea context.

Long-term variation in biodiversity and ecosystem function of abyssal megafauna

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There is now clear evidence that changes in climate and surface-ocean conditions can readily influence biogeochemical fluxes to abyssal depths. Variations in fluxes of sinking organic matter can lead to changes in community structure at the abyssal seafloor within days to months. The vast majority of the constituent organic carbon is ultimately metabolised and respired, buried in sediments, or recycled in marine food webs. The microbial and meiofauna portions of benthic communities are believed to be responsible for the majority of benthic respiration in the deep sea. We used new and existing abyssal megafauna respiration data to create a size-specific model of megafauna respiration. We then applied this model to time-series data on species-specific size and density of dominant megafauna from sites in the North-East Pacific and North-East Atlantic to estimate megafauna respiration variation over time. The respiration of megafauna was compared to respiration synchronously observed for the smaller sediment fauna as measured using respiration chambers inserted into the sediment. We found coherent interannual variations in megafauna respiration suggesting that climate variations also influence ecosystem function of large animals, even to abyssal depths.

Recruitment of deep-sea rose shrimp *Aristeus antennatus* (Risso, 1816) on Mediterranean bathyal habitats

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ICM-CSIC

The deep-sea rose shrimp *Aristeus antennatus* is an ecological and economical important species in the Mediterranean Sea and Atlantic Ocean. Its ecology and fishery have been studied during the past decades and its life history has been correlated to local geomorphological features such as the presence of submarine canyons and strong hydrographical events such as dense shelf downslope water cascading. It is a euribathic species that dwells from 100 to 2800 m in the Mediterranean waters. Recruitment to fishery of *A. antennatus* take place on the fishing grounds located at the submarine canyons walls. Mature females of *A. antennatus* are distributed at depths comprised between 500 and 900 m, but recruitment to habitat (composed by early juveniles) was unknown. Our present data, using bottom trawl surveys (OTMS otter trawl, benthic Agassiz trawl and a suprabenthic sled), support further information indicating that *A. antennatus* recruitment occurs mainly below 1000 m depth, but without any clear spatial zonation. This finding evidence that recruitment to habitat of the rose shrimp, seems not to be correlated to any oceanographic feature thus amplifying its area of recruitment along the vast bathyal bottoms.

Recolonization of experimental deployed sediments by meiobenthos organisms in an arctic deep-sea environment

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Commercial exploitation and an increasing disturbance frequency due to global climate change have severe impact on the arctic deep-sea ecosystem. Recolonization experiments are a reliable method to investigate the capability of an ecosystem to recover after a disturbance. The present study mimicked a situation after a disturbance in an Arctic deep-sea benthic environment and investigated if the recolonization by meiobenthos organisms is abetted by a certain nutrition and/ or sediment structure. Therefore, two “Sediment Tray Free Vehicles” were deployed in 2500 m water depth on the arctic deep-sea floor of the long-term observatory HAUSGARTEN of the Alfred-Wegener-Institute for one year. The chambers of the experimental devices were filled with different artificial and natural sediment types which were enriched with several types of nutrients. After one year, meiobenthos abundances and environmental parameters were investigated in the sediments. Observed meiobenthos abundances of originally defaunated sediments of the present recolonization experiments were similar to the individual numbers found in the surrounding deep-sea sediment after one year. Deep-sea sediment enriched with algae showed abundances closest to natural conditions. Foraminifera were the most successful group. They were dominant in all sediments and occurred with a relative frequency of 87% of the total meiobenthos in the sediments of the experiments. Individuals were generally smaller compared to the surrounding deep-sea sediment. Analyses of the environmental parameters revealed a significantly high correlation between meiobenthos abundances and chlorophyll a and phaeopigments, which are indicating fresh phytodetritus. Inferential, meiobenthos organisms can successfully recolonize azoic sediments after a perturbation event while the quality and quantity of the nutrition seemed to have a higher influence on the recolonization compared to the sediment structure.

Whale-fall community dynamics in Monterey Canyon, California, USA

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Whale carcasses that sink to the deep seafloor introduce a massive pulse of energy to a food-limited environment and give rise to dynamic communities of organisms. Seven years of observations on one natural and five implanted whale carcasses in Monterey Canyon showed that: (1) depth plays a significant role in species composition; (2) relatively common background taxa contribute substantially to the species richness of these communities; and (3) carcasses degrade very rapidly. Whales were surveyed using remotely operated vehicles (ROVs) equipped with studio-quality video cameras. All the observed and sampled organisms were identified to the lowest possible taxon and grouped by habitat association. Many new species were identified during this study, including 15 *Osedax* species, four provannid gastropods, several polychaete annelids and amphipod species. Nonetheless, the majority of species associated with these whale-falls are known and have been observed in other areas of Monterey Canyon. Bray-Curtis similarity analysis and multidimensional scaling revealed that whale-fall communities clustered primarily according to depth. Time-series mosaic images from the deepest whale-fall (Whale-2893) clearly illustrate rapid degradation over the course of seven years. Abundant *Osedax* bone-worms played a central role in accelerating the degradation of the bones.

The benthic fish fauna of abyssal plains in the Southern Atlantic

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Abyssal plains below 4000 m depth are by far the largest and least studied habitat on earth. Little is known about the abysso-benthic fauna, its species composition, distribution, and biogeography. Most studies on abyssal benthos were conducted in the North Atlantic, and only few studies were carried out in the South Atlantic. Thus, three recent expeditions of the German research vessel Meteor explored the abyssal plains of the South Atlantic. The cruises DIVA 1 (2000) and DIVA 2 (2005) visited the Guinea, Angola, and Cape Basin, while DIVA 3 (2009) focussed on the Argentine and Brazil Basin. The examination of the fishes obtained during these cruises and comparative studies of various museum collections provided new insights into biodiversity, species distribution, and biogeography of abysso-benthic fishes in the region. Demersal fish communities were dominated by macrourids (e.g. *Coryphaenoides* spp., *Echinomacrurus mollis*), ipnopids (e.g. *Bathymicrops regis*, *Bathypterois longipes*), and ophiidiids (e.g. *Abyssobrotula galathea*, *Bassozetus* spp., *Holcomycteronus profundissimus*, *Porogadus abyssalis*, *Barathrites iris*). Differences in community composition, species richness, and abundances among the basins are presented. Biodiversity and species distribution patterns are discussed with regard to basin-related productivity and latitudinal gradients.

Effects of carbon dioxide on deep-sea harpacticoids revisited

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As part of the evaluation of the environmental impact of sequestering carbon dioxide in the deep ocean, we exposed the sediment-dwelling fauna at a station in Monterey Submarine Canyon (36.378° N, 122.676° W, 3262 m) to carbon dioxide-rich seawater and found that most of the harpacticoid copepods were killed. In an expanded, follow-on experiment on the continental rise nearby (36.709° N, 123.523° W, 3607 m), not only did harpacticoids survive exposure to carbon dioxide-rich seawater, but we found no evidence from seven additional metrics that the harpacticoids had been affected. We infer that during the second experiment the harpacticoids were not exposed to a stressful dose. During the second experiment, carbon dioxide-rich seawater appears to have been produced more slowly than in the first, probably because of differences in the near-bottom flow regimes. We conclude that local physical circumstances can substantially influence the results of experiments of this type and will complicate the evaluation of the environmental consequences of deep-ocean carbon dioxide sequestration.

Long time-series measurements of benthic community processes to abyssal depths using an autonomous bottom-transiting vehicle

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MBARI

The deep ocean ecosystem covers two-thirds of the earth's surface yet its inaccessibility makes it poorly understood and grossly under-sampled. Long time-series monitoring is critical for measuring the impact of climate change in the deep ocean. We have developed the Benthic Rover, a bottom-transiting, autonomous underwater vehicle capable of making continuous time-series measurements of biological processes in the deep ocean to depths of up to 6000 m. This instrument was designed for long-term deployment as a cost-effective method of collecting continuous measurements of sediment community oxygen consumption (SCOC) at contiguous sites that capture changes occurring both seasonally and episodically. Measurements of SCOC are crucial to understanding the coupling between pelagic derived food supply and benthic community utilization of this organic carbon. The Benthic Rover is equipped with instruments developed to study sediment community activity at multiple sites. Two respirometer chambers on the front of the vehicle measure SCOC. Additional instrumentation includes a fluorometry system to detect phytopigment fluorescence (e.g. chlorophyll) on the sediment surface and three cameras that provide benthic images. The Benthic Rover can be deployed autonomously for up to six months with a programmable number of incubation sites or it can be tethered to an ocean observatory with real-time data collection and control. The Benthic Rover has completed 20 deployments in the Monterey Bay (~900 m depth) and at the deep-ocean time-series site Station M (4000 m depth) augmenting ongoing ecological studies. In 2009, a ten-week record of SCOC was collected while the Rover was tethered to the Monterey Accelerated Research System (MARS) cabled observatory at 980 m depth. During this deployment several serendipitous respiration measurements were made of three species of invertebrate megafauna and one demersal fish.

Continental margin biodiversity

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The Census of Marine Life has promoted synergetic approaches to assess and explain the diversity, distribution and abundance of life in the ocean, focusing on domains where new approaches allowed discoveries and new steps in Science. The field project "Continental Margin Ecosystems on a world-wide scale", COMARGE was launched in 2005 to address key issues on the ecology of continental margins, between the shelf break (~20 m) and the abyssal plain (~4000 m). This realm is now known to be biologically rich with unique habitats including canyons, oxygen minimum zones, cold seeps and reef like coral mounds better explored owing to the development of new oceanographic equipments. In an attempt to merge known but unexplained ecological patterns with new discoveries and development, COMARGE focused on three main questions:

- Are large-scale biodiversity patterns such as zonation or diversity-depth trends ubiquitous and what are their drivers?
- What are the margin habitats and what is the relationship between diversity and habitat heterogeneity?
- Is there a specific response of continental margin biota to anthropogenic disturbances?

A network of scientists, now gathering over a hundred, has promoted discussions and syntheses through four thematic workshops. Data integration was achieved either through the Ocean Biogeographic Information System (OBIS, www.iobis.org) or via the COMARGE Information System (COMARGIS) ecologically orientated. The synthetic results on a world wide scale allow to demonstrate that depth zonation is ubiquitous along continental margins; that the diversity reaches a peak at mid-slope depth except for oxygen minimum zones, that heterogeneity acts in a hierarchical scale-dependent manner to influence margin diversity: - at meso scales (10s km) there is topographic control in the form of canyons, banks, ridges, pinnacles, and sediment fans; - at smaller scales there are earth and tectonic processes that control fluid seepage and sediment disturbance; - at the smallest scales there are habitats formed by ecosystem engineers that influence diversity through provision of substrate, food, refuge and various biotic interactions. These results will be discussed and put in perspectives with major remaining unknowns that, among other issues, still limit our ability to predict the consequences of increasing anthropogenic threats on continental margin ecosystems.

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Larval transport modelling of deep-sea invertebrates points to potential undiscovered populations

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This research presents a novel combination of data and methodology to study the potential connectivity of deep-sea benthic populations, in a test case applied to the known distribution of four species of deep-sea chitons in the south-west Pacific, found on sunken wood from 200 – 1600 m. The species are well defined by multiple morphological characters, and are known to range on sunken wood across the whole of the tropical Pacific. Our analysis makes a quantitative estimate of the probability that the known populations of these four chiton species can be directly connected by larval transport. Our model infers larval dispersal capability by combining oceanographic, species distribution and physiological data. Dispersal speed and direction are estimated from ARGO probe data; dispersal times are inferred from comparative (shallow water) and predicted (temperature-based estimates) larval lifespans. Finally, the release locations of the larval particles are based upon species distribution data from deep-sea ecological surveys. This information is combined into a coupled biophysical larval transport model, which predicts the likely dispersal pathways of larvae. Our analysis shows that direct connectivity is unlikely between the three archipelagos where the deep-sea chitons have been found because the spatial scale of simulated larval dispersal is an order of magnitude too small and dispersal directions carry larvae away from the known populations. In considering mechanisms that could connect the known conspecific populations, we consider the most parsimonious explanation to be a large number of intermediate habitats which have not yet been discovered; our modelling approach can be used to produce testable hypotheses about the density and the likely locations of these intermediate stepping stone populations.

Investigations of the diversity and substrate specificity of Pacific seamount zoanthids

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Zoanthids (Cnidaria, Hexacorallia) are distributed in all marine environments from the deep sea to the intertidal and from the Antarctic to Arctic. Identification of zoanthid species based on histological and morphological characters has always been difficult and controversial. Because of these difficulties, this group of anthozoans is regularly ignored in diversity and ecological surveys. Molecular methods have proved helpful to investigating shallow water zoanthid diversity. However, most diversity is expected to be found in deep sea environments. Thus information from the deep-sea taxa is essential to understand the biology and evolution of this group. This study used a DNA barcoding approach to clarify the taxonomic diversity of the Zoantharia from Hawaiian and New Zealand seamounts. We compared the taxonomic resolution and variation of 4 genetic markers in relation to the taxonomy and evolutionary hypotheses recently developed for zoanthids. Preliminary phylogenetic results suggest a need to reconsider some traditionally used morphological characters (e.g. the secretion of an axis in the genus *Savalia*). Instead, substrate specificity appears to be tightly linked to the evolution

of this group. The investigation of deep seamount zoanthid biodiversity throughout the Pacific revealed an important unknown diversity of octocoral-associated zoanthids which further support this hypothesis.

High megabenthic abundance and diversity in deep fjords of the West Antarctic Peninsula: high sensitivity to climate change?

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Fjords provide deep-sea, soft-sediment habitats in proximity to coastal productivity. Fjord-floor communities in boreal regions are relatively well studied and often are disturbed, low diversity systems suffering from sediment loading and/or hypoxia. Benthic ecosystems in the polar-subpolar fjords along the West Antarctic Peninsula (WAP) remain poorly studied even though they are among the most extensive fjord habitats in the southern hemisphere. To evaluate benthic abundance and biodiversity in the deep WAP fjords, we conducted seafloor photographic surveys and limited megacore sampling at 450 – 600 m in middle, inner and outer basins of four fjords: Hughes, Flandres, Andvord and Barilari Bays. Photographic surveys revealed extraordinary megafaunal abundance and species richness at the fjord floors with megafaunal abundances ($7.1 - 10.2 \text{ m}^2$) 4 – 6 time greater than at similar depths on the open continental shelf. Megabenthic species richness on soft sediments in single fjords exceeded 100 species, while comparable depths on the open shelf yielded ~60 species. Megacore samples suggest similarly high biomass and biodiversity for the fjord macrobenthos. In addition, macrofaunal body sizes were unusually large in the fjords, and multiple species exhibited ripe reproductive condition and extraordinary fecundity. Seafloor photographic surveys also indicated high abundance of drift macroalgae on the fjord floors. Our results suggest that the WAP fjords are hotspots of benthic productivity and biodiversity, sustain different food inputs (e.g., macroalgal detritus) than the open shelf, and may be important larval sources for the broader WAP shelf. These patterns contrast sharply with fjord systems in warmer regions, where much greater glacial inputs of melt-water and till often reduce water-column productivity and cause intense sedimentation disturbance of benthos. Because glacial melt-water and till inputs are increasing in the WAP fjords with climate warming, these fjord hotspots of biomass and biodiversity and may be substantially impacted by climate change.

Unlocking mineral resources from the deep seafloor: environmental Considerations

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Nautilus Minerals is following the lead of the petroleum industry as it attempts to tap vast offshore resources. Planning is underway for the high grade Solwara 1 Seafloor Massive Sulphide Project in the Bismarck Sea, Papua New Guinea (PNG), at ~1600 m water depth. The deposit contains an average copper grade more than ten times higher than a typical land-based porphyry copper mine, as well as a significant high grade gold credit. The high grades combined with a relatively small amount of overburden ensure the Solwara 1 Project will have a significantly smaller physical footprint than its land-based counterparts. Other

advantages include little social disturbance, increased worker safety (operations will be carried out remotely) and the development of previously unutilized “zero value” resources.

Several strategies to minimize the environmental impacts of the Solwara 1 Project were recommended by the project’s science advisors, and are on track to be developed in the mine operation plan. Impacts to surface waters have been engineered out, with no mining discharges at the surface and no chemical discharges during the mining process. At depth, the primary impact is the removal of material and habitat from the seafloor. Several impact minimization strategies have been proposed to the PNG government, such as: setting aside an area of the seafloor “upstream” of Solwara 1, establishing temporary refuge areas within Solwara 1, relocating some animals out of the path of mining and placing them where mining has already occurred, installing artificial substrates, among others.

This paper will outline the leading edge approach Nautilus has taken in completing the environmental impact statement for the world’s first deep seafloor copper-gold mine. In addition, this paper will review the permitting process and the government and stakeholder engagement undertaken as part of Nautilus’ desire to “do it right” in this exciting new industry.

Dropstones: sources for habitat heterogeneity in the deep Arctic Ocean

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Dropstones are the product of distinct entrainment and transport mechanisms, e.g. ice rafting (icebergs and ice-flows as rafting agents), biological rafting (single stones or clusters of stones carried by tree roots, and stomach-stones), physically propelled deposition (projectiles of volcanic origin) as well as floatation and gravitational processes (restricted to relatively small particles). Like sunken wood, whale bones or human debris, dropstones at the deep seafloor form concrete “islands” in a soft-bottom environment. In contrast to sunken objects in near-shore environments, hard substrata in bathyal and abyssal depths are not affected by physical disturbance such as rock turnover.

Dropstones interact with near-bottom currents and modify local flow patterns, thereby altering particle deposition and erosion rates. As a result, surface-derived detrital organic matter, which is an important food source for benthic organisms, is trapped in or around these structures. Accumulated organic matter on the leeward side of projecting structures is expected to affect distribution patterns of the smallest benthic organisms (i.e. bacteria, fungi, ciliates, flagellates, protozoans, small metazoans), as already demonstrated for shallow-water habitats and deep-water habitats. In this respect, dropstones may constitute a source of habitat heterogeneity in marine environments.

During an expedition to the deep-sea long-term observatory HAUSGARTEN in eastern Fram Strait, the availability of a Remotely Operated Vehicle allowed the targeted sampling of surface sediments around a large dropstone of approximately 60x150 cm and up to 15 cm in height, to determine suspected differences in activity, biomass, and diversity of the small sediment-inhabiting biota in relation to the confined flow regime and a supposed patchy food availability in the immediate vicinity of the stone. The aim of this study was to test the hypothesis that dropstones, as sources of habitat heterogeneity in a marine soft-bottom environment, may contribute to enhanced biodiversity of small benthic organisms in the deep-sea realm.

Variations in benthic community structure, abundance and diversity along an Antarctic latitudinal sea ice gradient

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The West Antarctic Peninsula (WAP) is warming as fast as any region on Earth, reducing sea-ice cover, changing primary production, and altering pelagic-benthic coupling. However, the effects of sea-ice duration on benthic community structure have not been studied on the deep (500-1000 m), sediment covered Antarctic continental shelf. We studied benthic community structure at five physically similar midshelf stations (550–650 m depth) along a strong latitudinal gradient in annual sea-ice duration from Smith Island (63°S) to Marguerite Bay (68°S). Analysis of remote sensing data indicates that average annual sea-ice duration varies from <1 month at our northernmost station (Sta. AA) to >7 months at the southernmost station (Sta. G). Megacore samples (n = 5) from each of the five stations elucidated changes in macrofaunal abundance, community structure and diversity along the sea-ice gradient. Community structure at all stations was dominated by polychaetes, followed by crustaceans and bivalves. Mean macrofaunal abundances were relatively high, ranging from 13,125 – 18,675 individuals per m². However, we found no obvious trends in macrofaunal abundance versus sea-ice duration, with a middle station (B at 64°S) exhibiting the lowest abundance and the most northerly and southerly stations showing the highest. This suggests sea-ice duration and other latitudinally varying parameters are not strong regional drivers of macrofaunal abundance along the WAP shelf. However, a strong latitudinal trend was observed in community structure, with community dominance by Spionidae polychaetes increasing from 35% to 48% from the north to south ends of our transect. Spionid dominance was driven by a single, recently described species, *Aurospio foodbanesia*, with an abundance of 29-45% of total macrofauna. We speculate that *A. foodbanesia* dominates because of an ability to respond to rapid shifts in food availability from production pulses, allowing it to be the most abundant macrofaunal species on the Antarctic shelf.

Population connectivity in a biostructuring hydrothermal vent tubeworm

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Ridgeia piscesae is an important biostructuring species at hydrothermal vents in the northeast Pacific Ocean. This vestimentiferan tubeworm is phenotypically plastic, displaying a range of morphologies depending on the environment it inhabits. *R. piscesae* lives in symbiosis with sulphur oxidizing bacteria that use sulphides from hydrothermal vent fluid to fix carbon, that is subsequently translocated to the host. Vent fluid flux is highly variable in both time and space in this environment, leading to variability in the energy available to *R. piscesae* for growth and reproduction. *R. piscesae* is a foundation species in communities that it inhabits, making it a prime subject for the study of population connectivity at hydrothermal vents in the northeast Pacific Ocean. This study tested the hypothesis that tubeworms from both high and low flux habitats contribute equally to the larval pool and that larvae arrive equally in both habitats. Over 400 tubeworms from 9 pairs of high and low flux habitat were examined using

morphological and histological methods. These were rated for adult condition, reproductive condition, and juvenile abundance on adult tubes. I found substantial differences in reproductive potential among high and low flux habitat. There was a significantly higher incidence of mature individuals in high flux habitat. Tubeworms experiencing high fluid flux had significantly higher body weights, more lipids per unit body weight, and larger gonads with far more gametes present than those in low flux patches. There was also some variability in the abundance of juveniles recruited onto adult tubes. These results suggest that there are “source” and “sink” habitat types in the highly fragmented population of *Ridgeia piscesae* in the Endeavour Hot Vents Marine Protected Area. If this is the case, there are implications for population genetic structure, as effective population size will be much smaller than actual population size.

Sequencing and analysis of a multiple tissue-specific transcriptome from the black cabbardfish, *Aphanopus carbo* (Perciformes: Trachiuridae) using 454 technology

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A multiple small-scale transcriptome study has been undertaken for *Aphanopus carbo*, deep sea species known for its commercial values and intriguing phylogeny of its genus. The sequencing and analysis of several thousands of expressed sequence tags (ESTs) from this species is presented. ESTs were derived from cDNA of non-normalised libraries of six different tissues (muscle, heart, liver, spleen, brain and gonads). Multiple approaches are applied to assign putative function to each transcript; sequence homology searches using BLASTX (Basic Local Alignment Search Tool: Translated query versus protein database) of the National Center for Biotechnology Information’s (NCBI) GenBank Database and Gene Ontology annotation. The sequence and complete annotation of all ESTs is under scrutiny before becoming available to a publicly accessible database. This is the first deep-sea fish transcriptome database based on the 454 pyrosequencing technology and this study is a prelude to an even larger effort aimed at exploring more cDNA libraries from other deep-sea fishes toward the goal of understanding adaptations of Teleosts to the deep sea.

Dominant species of the genus *Calanus* in the North Atlantic: species range limits significantly moved to South

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Three species of the genus *Calanus* – *C. hyperboreus*, *C. finmarchicus*, *C. helgolandicus* – are indicators of the water masses. Their native habitats are the arctic, temperate, and subtropical North Atlantic waters, respectively. Distribution of these species was studied along the North-Atlantic Ridge within the depth range 0–3000 m. A total of 16 vertical plankton net series (10 sites) between 23° N and 55° N were made during Cruises of R/V “Akademik Mstislav Keldysh” and R/V “G.O.Sars” (MarEco Programme). Material was sampled with the BR plankton net (mouth area 1 m², mesh size 500 µm) and Multinet (mouth area 0.25 m², mesh size 200 µm). South range limits of *C. hyperboreus* and *C. finmarchicus* were recorded at 30°

N and 23° N, respectively; *C. helgolandicus* was recorded everywhere being most abundant at 37° N. The Southernmore species recorded, the deeper they lived. Our data were compared with the earlier extensive material of Sars (1925), Kanaeva (1960), Yashnov (1961), Fleminger & Hulsemann (1977); Planque & Batten (2000) in order to trace temporal changes in the species range limits. Comparison showed that the species of *Calanus* are distributed along the North-Atlantic Ridge by deep-sea currents far away from the main habitat. Recent collections indicate that the species range limits significantly moved to South. The arctic species *C. hyperboreus* found now at 30° N has never been recorded southernmore than 53° N. The temperate species *C. finmarchicus* now found within the North Atlantic cyclonic gyre at 23° N has never been recorded before southernmore than 28° N. The subtropical species *C. helgolandicus* now found farther in the Southwest direction than before and its distribution to North is now restricted by the latitude 48° N instead of 65° N. Thus, the southern and northern range limits of the dominant species of *Calanus* have significantly moved to South that may reflect changes in the oceans circulation.

Planulation patterns, larval development, settlement and early growth of deep-sea octocorals from the northwest Atlantic

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We present laboratory data on the timing of larval release, development, substratum selectivity and growth of several alcyonaceans (Cnidaria, Octocorallia) from the bathyal zone of eastern Canada. Species under study included *Drifa glomerata*, *Drifa* sp., *Gersemia fruticosa* and *Duva florida* collected between 100 and 1240 m depth. They were monitored for over a year in flow-through systems maintained in darkened conditions. Planulation persisted for several months in the larger more fecund colonies, but peak events in most species were significantly influenced by seasonal factors including seawater temperature and productivity. Clear lunar patterns were determined in *G. fruticosa* and *Drifa* sp. Planulae of the different species exhibited a wide range of sizes and behaviours. Settlement trials showed that planulae of *Drifa* spp. settled more readily on hard rough surfaces covered with biofilms than on all other substrata tested and that larvae of colonies from deeper habitats were less selective than those originating from shallower habitats. Planulae of *Duva florida* that were extracted surgically from several colonies metamorphosed and settled like the naturally released ones. A common trend in the species studied is that metamorphosis and settlement could occur within a day after release or be delayed for several weeks. The eight primary mesenteries typically appeared within 24 h post settlement and primary polyps grew to a maximum size in 2–3 months. Budding was rare in primary polyps that were monitored for 11 to 21 months post settlement, suggesting a very slow growth rate. This appears to be somewhat compensated by precocious sexual maturity, as shown by the presence of planulae in small colonies composed of only 10–25 polyps.

Environmental conditions at a deep sea site proposed for commercial development: Solwara 1, Papua New Guinea

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Solwara 1, a seafloor massive sulphide deposit in the Bismarck Sea (~1600 mbsl), Papua New Guinea, is being proposed by Nautilus Minerals for commercial development. Through collaborations with science, the baseline environment has been well defined. Two 30-day ROV campaigns collected >450 biological, sediment and water samples and logged >22,500 seafloor observations, making Solwara 1 the most comprehensively studied hydrothermal vent field in the Manus Basin.

Dormant and actively venting areas are present and both were studied. Dominant macrofauna inhabiting dormant sulphide substrate include *Keratoisis* sp., *Vulcanolepas parensis*, *Abyssocladia* sp. and various hydroids. Active vent sites are dominated by three species (2 gastropods: *Alviniconcha* sp, *Ifremeria* sp. and a barnacle: *Eochionelasmus* sp.). Tanids and nuculanoid bivalves are the dominant taxa of infauna associated with both active and dormant sites. Solwara 1 exhibited low faunal densities and biomass in comparison to other hydrothermal systems worldwide.

Solwara 1 is a dynamic environment subject to natural disturbances and variations. As a result of subsea volcanic emissions, ambient sedimentation rates at Solwara 1 are about 2.3 times higher than the global oceanic average. The venting fluid is metal rich and ambient water near vents fails to meet water quality guidelines. Visual comparisons of sites visited over multiple years showed local scale changes to venting. Biological communities must be tolerant and/or adaptable in order to survive.

Visual observations of patches of apparently dead gastropods may indicate venting cessation and/or the movement of gastropods in search of venting fluid. Vent dependent gastropod species were seen moving towards actively venting areas. Formation of new chimney lattice material was also observed in as little as 21 hours after sampling, which in combination with the fauna's apparent ability to cope with a naturally variable environment, implies active vent sites at Solwara 1 are resilient to disturbance.

Deep-sea meiofauna communities and associated biogenic structures in the NE Pacific

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Because of the trifling photosynthetic rates, deep-sea organic matter availability regulates benthic productivity and biomass. Previous time-series monitoring at the sampling site in the NE Pacific (Station M) revealed a coupling between the maximum flux of particulate matter entering the benthic boundary layer and the presence of detrital aggregates on the sea floor. Seasonal inputs of phytodetritus appeared to be an important food source for epibenthic fauna at station M, thus affecting their community structure in both space and time. Furthermore, global warming has been predicted to intensify stratification and reduce vertical mixing, thus enhancing variability in primary production and carbon export flux to the deep sea. The dependence therefore of deep-sea communities on surface water production raises important

questions regarding how climate change will affect cycling and deep-ocean function. With this in mind a series of dives with the submersible ALVIN were undertaken at station M in August 2006 to investigate, among other things, the micro-habitat distribution of meiofauna. Twelve microhabitats were sampled at 4100 m depth, which were: a) control, b) within the track of *Echinocrepis* urchin, c) outside the track of *Echinocrepis* urchin, d) within the track of *Cystocrepis* urchin, e) outside the track of *Cystocrepis* urchin, f) on a bioturbation mound, g) along the periphery of the bioturbation mound, h) away from the bioturbation mound, i) away from a sponge, k) near the stalk of a sponge, l) near a decomposing kelp holdfast and m) away from the kelp holdfast. Total meiofaunal abundances ranged from 244 to 1203 individuals 10 cm². The station away from the sponge exhibited the highest values while the bioturbation mound had the lowest. Nematodes were the dominant group, ranging from 71 to 89%, followed by harpacticoid copepods and polychaetes. The other groups were represented on average with less than 6%.

Using DNA taxonomy to estimate octocoral diversity: the search for octocoral's silver-bullet(s)

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Octocorals are associated with coral gardens that may form vulnerable marine ecosystems that are impacted or potentially impacted by deep sea bottom fisheries globally. However, octocorals are understudied and their taxonomy is poorly resolved. The number of octocoral taxonomists globally is very low, the time required to gain taxonomic experience lengthy to the tune of decades, and the time required to correctly identify the often morphologically plastic specimens is also moderately protracted. As morphological taxonomy is very time consuming, DNA-based taxonomy is thus suggested as a solution to locating areas of high octocoral diversity in the deep-sea.

In South Georgia octocorals formed the majority of by-catch in the Patagonian toothfish bottom longline fishery, with the dominant taxa being primnoid octocorals from the genus *Thouarella*. These octocorals are locally abundant in many areas of the deep sea, especially in the sub Antarctic, and may play an important ecological role as habitat for other species. Though relatively common, little research has focused on *Thouarella* species identifications beyond the original type descriptions, many of which are from the turn of last century. Here a summary of a new revision of *Thouarella* is presented. Studies of 35 type specimens of the initial 38 *Thouarella* species, two varieties and one form, reduced the number of *Thouarella* species to 25, mostly through synonymisation or new generic combinations.

The *Thouarella* revision makes it possible to compare morphological species information against genetic information. In this manner the efficiency of three genetic markers at discriminating species was investigated within *Thouarella* and more widely within Primnoidae. Studies on the diversity of octocorals in by-catch will be used to reassess MPA placement around South Georgia and inform fisheries management.

Megabenthos diversity patterns in the deep Mediterranean along depth and west-to-east axes

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The Mediterranean deep-sea environment is a unique natural laboratory to study ecological processes, presenting a marked western-eastern gradient of decreasing primary production. Commercial trawling reaches depths of 900 m maximum, allowing for studies of non-impacted environments below this depth. Knowledge of benthic megafauna diversity, its patterns of variation between basins and the response of megafauna to environmental conditions are at present very scarce. Sampling was conducted with a commercial benthic otter-trawl (OTMS) and an Agassiz dredge was conducted in 5 cruises in 2009, in the Catalan Sea slope, the Southern Balearic Sea, the Western Ionian Sea and South of Crete, at depths of 900-4000 m. Abundance, biomass and diversity patterns of all megafauna were analyzed. Depth was confirmed as the strongest influencing factor for community composition, both at large scale between the three basins (1200-2000-2800 m) and at small scale in the lower Catalan slope (900-1500 m at increments of 150 m). Differences in species composition were found also between the Catalan slope and the adjacent Blanes submarine canyon. Abundance and biomass decreased with increasing depth, and also in a western-eastern gradient. Diversity was to a large extent constant in the Southern Balearic Sea with decreasing depth, suggesting that organic matter arrival at the deep basin permits a stable diverse community even at 2800 m depth. In the South of Crete, diversity decreased between 1200 and 2000 m. The Western Ionian Sea, traditionally considered as presenting transitional characteristics between the Western Basin and the highly-oligotrophic Eastern Mediterranean, showed a similar diversity between 1200 and 2800 m depth.

The role of specific dynamic action in the hydrostatic pressure tolerance of the shallow water spider crab *Maja brachydactyla*

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The bathymetric distribution of marine benthic invertebrates is likely governed by a combination of ecological and physiological factors. The present study investigates oxygen consumption and heartbeat rate in response to attempted feeding at 1, 100, and 150 atm in the shallow water spider crab, *Maja brachydactyla*, from temperate European waters. No significant difference was evident between the resting heartbeat rate of specimens at 1 or 100 atm, which were 56 and 65 bpm, respectively (Mann-Whitney: $U = 5382.0$, $n = 95, 98$, $P = 0.079$). However, at 150 atm the resting heartbeat rate was significantly higher than that observed for 100 atm at 108 bpm (Mann-Whitney: $U = 149.0$, $n = 45, 98$, $P < 0.001$). At 150 atm feeding was never observed and coupled with the elevated resting heartbeat rate; it is suggested by 150 atm continued survival is unfeasible. At 1 and 100 atm feeding instigated a distinct increase in heartbeat rate, which remained elevated for over 30 h. This increase peaked within 1 h at 1 atm. At 100 atm this required 4 h and postprandial oxygen consumption was significant higher than at 1 atm (Kruskal-Wallis: $H = 85.036$, $d.f. = 2$, $P < 0.001$). Elevated hydrostatic pressure is hypothesised to extend the duration and the total metabolic energy devoted to specific dynamic action. The results indicate that the

physiological scope of hydrostatic pressure in temperate marine invertebrates inhabiting the continental shelf may likely exceed their natural depth distribution range. The observations are discussed with respect to the likelihood of invertebrates to escape warming of surface waters by submerging into deeper waters.

Recent insights on siboglinid phylogeny, symbiosis and evolution

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Siboglinids are a clade of annelids obligately dependent on microbial endosymbionts for nutrition. The clade includes four main groups: the former Pogonophora (aka Frenulata) and Vestimentifera, the bone-eating *Osedax* and organic-loving *Sclerolinum*. Whereas much attention has been given to vestimentiferans and, recently, *Osedax*, frenulates are much more diverse but have received only limited attention. We are re-examining siboglinid phylogeny using multiple genes, with an emphasis on frenulate diversity and the position of *Osedax*. Additionally, we are using a transcriptome-based approach to understand physiological interactions (from the host perspective) between the animal host and its bacterial endosymbiont(s). Specifically, the transcriptomes of hydrocarbon seep vestimentiferans are being examined with 454 pyrosequencing to elucidate genes expressed in host tissue as well as within the endosymbionts. Additionally, we are expanding sampling of endosymbionts in frenulates to obtain a more complete understanding of their phylogeny. Through examination of different symbiont/host partnerships we hope to address interesting questions about host/symbiont fidelity over the course of evolution.

Integrative biology of a ‘model species’, *Adipicola iwaotakii*, associated with sunken organic substrates

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Despite the number and the diversity of the studies available, the evolutionary origin and processes explaining the diversification of deep-sea chemosynthetic fauna remain poorly understood. In this context, the Bathymodiolinae are a model sub-family because they are part of the dominant fauna from these environments. Based on phylogenetic studies, the Bathymodiolinae, initially described for hydrothermal vents, was shown to belong to the same clade than poorly-known species associated with sunken organic substrates. Moreover, a close relationship was displayed between a lineage that includes exclusively vents and seeps species, named “*thermophilus*”, and a lineage that not includes vent species but mostly species from organic falls. Thus, to better understand the evolutionary processes in chemosynthetic environments, an integrative study of the biology of a species inhabiting organic falls was carried out. Indeed, whereas the biology of vents and seeps species are relatively well documented, that of the small mussels of sunken wood is largely unknown. A

species belonging to the sister-clade of “*thermophilus*” lineage, *Adipicola iwaotakii*, is chosen here to document their life-history traits and population structure. Nutritional strategies of this ‘model species’ was assessed by examining the bacterial diversity (based on 16 rRNA gene, TEM and FISH) coupled with the analysis of the digestive tract from microscopic data. Anatomical observations showed that digestive tract was complete contrarily to some Bathymodiolinae which have often reduced but functional digestive-tract. Our study of the bacterial diversity allowed detecting thiotrophic ectosymbionts close to those identified in Bathymodiolinae. Observations of prodissoconchs suggest high dispersal abilities. Genetic structure analyses, performed with a mitochondrial gene, exhibited a North-South structure throughout South-Western Pacific but no structure considering various sunken organic substrates. The comparison of these data to model species from vents (i.e *Bathymodiolus thermophilus* and *B. azoricus*) highlights the evolutionary processes that explain the colonization of vent environments.

Dancing for food in the deep-sea: a unique symbiosis by a novel species of yeti crab

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The deep sea remains largely unexplored and hosts a diversity of unknown species. During exploration of a methane seep off Costa Rica, we discovered the second species of “Yeti Crab”, a member of the newly described family Kiwaidae. Video footage showed these crabs conducting a unique behavior of waving their chelipeds (first walking legs) in areas of active seepage. Subsequent microscopic and molecular analyses demonstrated that these chelipeds were covered with filamentous bacteria. Phylogenetic analysis of the bacteria indicated that the epibionts were most closely related to hydrothermal vent inhabiting decapod symbionts. Stable isotopic and fatty acid biomarker analyses also found that chemosynthetic production was the main source of nutrition for this crab species. Also, similar biomarkers between the tissue and the bacteria-dominated spines suggested that the epibiotic bacteria on the chelipeds are farmed by this novel crab species for nutrition. Modified setae on the 3rd maxilliped (mouth appendage) provided evidence for a potential mechanism for bacteria harvesting, and both in situ and laboratory observations showed the crabs using these appendages to scrape their bacteria-laden setae. We hypothesize that the crab’s arm waving behavior is a mechanism to increase the availability of hydrogen sulfide and oxygen to its symbionts and increase the crab’s epibionts chemoautotrophic production. As the closest relatives of this new species and its epibionts are from hydrothermal systems, this discovery of a methane seep *Kiwa* provides an example of the close relationship among the deep-sea reducing ecosystems. In addition, the close evolutionary relationship of these symbionts across ocean basin and chemosynthetic ecosystem supports the hypothesis that there is a microbial community which specializes as epibionts of reducing habitat decapods.

Discovery of new faunal sites on the EPR (16°N): abyssal, bathyal and hydrothermal communities

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The PARISUB cruise is a multidisciplinary and international research project with the purpose to explore with a manned submersible the area between 15°N -16°N and 105°E-106°E where EPR interacts with hotspots (Mathematician hotspot chain). The objectives are to study the axis instabilities, to sample the basalts across and along axis and to identify the type and the evolution of volcanism by a very high precision bathymetry and on bottom magnetic anomalies and to locate possible hydrothermal vents. Components of faunal communities in the area would serve as indicators of biodiversity and of specific substrates and environmental characteristics. From 24 dives (110h) with the Nautilie and 20 dives (112h) of the prototype AUV ASTER X, geological, including geophysical (magnetism and bathymetry) and biological surveys have been achieved over 122 km². A great amount of samples of lava (about 1 ton), 6 fossil chimneys and fauna (more than 250 samples among which DNA samples) have been collected. A new active hydrothermal area including a variety of faunal communities adapted to specific thermal and geochemical conditions has been discovered among which 2 diffuse flow vents and 2 black and white smokers have been explored and sampled more thoroughly. The exploration was between 4500m and 2300m depth revealing abyssal and bathyal faunal communities. Abundance and biodiversity was higher on heavily sedimented rocky substrate composed of basalt with metalliferous crusts, mainly manganese. Sediments were highly populated by meiofauna and macrofauna. On the slopes of pillow lava, faunal communities were often suspension feeders with a mixture of abyssal and bathyal species. Abundance and taxonomic richness was much lower on the fresh lava on the axis. Active hydrothermalism was discovered over an area with a mosaic of conspicuous faunal communities adapted to specific environmental, thermal and geochemical conditions including two areas of diffuse vents and two of black smokers which have been investigated and sampled more thoroughly. There seems to have a linear arrangement parallel to the axis: along the wall of the narrow axial valley on the west are the active and fossil smokers, then when going eastwards one would encounter first sulphide deposits, then diffuse vent biota and associated biocenoses in the vicinity. It is a priority to increase knowledge on these hydrothermal biocenoses in order to draw guidelines for the conservation of their biodiversity before they would be destroyed by mining companies in the near future.

Endemism at low sampling effort: real or artifact?

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High rates of apparent endemism have been found in some deep-sea environments such as seamounts and cold-seeps. Yet these environments are often chronically undersampled, with samples that are small in scale drawn from populations that can be widely separated in space. Given the importance of endemics in influencing conservation and management decisions, it

seems valuable to gain an understanding of how the level of sampling effort might affect estimates of endemism.

We used simulations to explore whether 'true endemism' was distinguishable from artifacts induced by incomplete sampling. Identical populations, comprising the same species in the same proportions, were generated and then sampled from at varying intensities. We then assessed the proportion of 'false' endemics, i.e. those species apparently present in only a single population due to insufficient sampling. The level of 'false' endemism depended heavily on both community evenness and sampling effort. These models were then applied to abyssal data from the central Pacific to assess whether the level of sampling effort was sufficient to eliminate such 'false' endemics (i.e. artifacts of limited sampling). We found that an order of magnitude greater sampling effort than that conducted was necessary to have reasonable confidence in observed levels of apparent endemism. This level of sampling is currently impractical for seamounts and other remote or challenging environments, thus raising doubts over present estimates of potential endemism. The modelling of endemism at low levels of sampling intensity, and the level of sampling necessary to quantify estimates with reasonable precision, could prove to be a useful tool for biodiversity management and conservation.

Estimating *Synaphobranchus kaupi* densities: contribution of fish behaviour to differences between baited camera and strip transects

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Ifremer

The northern cutthroat eel *Synaphobranchus kaupi* is a small-bodied, abundant inhabitant of the European continental slope. To estimate its local density and derive its preferred habitat, we collected video information using a remotely operated vehicle at three locations in the Bay of Biscay (1100–1500 m). Two methods for estimating local densities were tested: strip transect counts and point counts with and without baits. During strip transects the observation field was calibrated allowing absolute density estimates to be derived. Local densities were found to vary between sites, depth, current speed and day and night. Further, the spatial distribution of individuals was aggregative. Twenty-four bait experiments were carried out spread evenly across the depth range. Two types of bait were tested: fish farming pellets with sardine oil and pieces of cod. For all individuals time of arrival and behaviour type was noted. Four feeding types were observed: moving up the current towards the ROV (36%), moving across the current (31%), drifting with the current (32%) and sitting motionless (<1%). The proportion of individuals showing each feeding type did not depend on local conditions (temperature, current speed or depth). Visible attraction towards the bait was highest for individuals swimming against the current (80%) and about equally low for those moving across current (40%) or drifting (30%); it increased slightly with temperature and depth. Using a simple model for odour plume diffusion and assumptions regarding swimming speed, local densities at least 10 times smaller than those estimated by strip transects were obtained. A hierarchical Bayesian model allowed then to integrate prior knowledge on behaviour and the data from the two types of point counts to estimate local densities when not all individuals react and individuals are not randomly distributed, making estimates from bait counts and strip transects more similar.

The cold-water coral community as a hotspot of carbon cycling on continental margins: a food web analysis from Rockall Bank (Northeast Atlantic)

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The carbon flows in the food web of the cold-water coral community associated with the reef-building *Lophelia pertusa* at ~800 m depth at Rockall Bank was quantified using linear inverse modeling. Quantitative data on biomass, on-board respiration of different compartments, $\delta^{15}\text{N}$ values, and literature constraints on assimilation and growth efficiencies were available. The carbon flux to the coral community was $75.1 \text{ mmol C m}^{-2} \text{ d}^{-1}$ and was partitioned among (phyto)detritus (81%) and zooplankton (19%). Carbon ingestion by the living coral was only 9% of the carbon ingestion by the whole community and was portioned among (phyto)detritus (72%) and zooplankton (28%). Carbon cycling in the community was dominated by suspension and filter-feeding macrofauna associated with dead coral branches. Sediment traps mounted on a bottom lander trapped $0.77 \text{ mmol C m}^{-2} \text{ d}^{-1}$ (annual average), which is almost two orders of magnitude lower than total carbon ingestion (75.1) and respiration ($57.3 \text{ mmol C m}^{-2} \text{ d}^{-1}$) by the coral community. This discrepancy is explained in two ways: the coral community intercepts organic matter that would otherwise not sediment, and as ecosystem engineers, the increased turbulence generated by the coral framework and organic matter depletion in the boundary layer augments the influx to the coral community. A comparison of the biomass and respiration data with soft-sediments reveals that coral communities are hotspots of biomass and carbon cycling along continental margins. The results from Rockall Bank will be contrasted against recent food web analysis of the Atlantic cold-water communities at Hatton Bank and Mingulay reef.

The cirrate-octopod assemblage of the Charlie-Gibbs Fracture Zone, Mid-Atlantic Ridge

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Cirrate, or finned, octopods are primitive deep-sea cephalopods. They are also called "dumbos" in popular accounts because they swim by flapping a pair of ear-like fins on the sides of their bodies, making them look like the cartoon flying elephant. Multiple cruises by the MAR-ECO project of the Census of Marine Life have documented a multi-species assemblage of these "dumbos" associate with the mid-Atlantic Ridge, especially in the area of the Charlie-Gibbs Fracture Zone. This assemblage includes nine species, one of which may be new to science, in three families. The specimens collected included both rarely collected species and large animals, up to 1.5 m in total length and some were among the largest ever reported.

Comparative symbiont diversity in the bone-eating worm *Osedax* from shallow and deep-sea whale-falls

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Osedax worms are whale-fall specialists that infiltrate whale bones with their root tissues. These are filled with endosymbiotic bacteria hypothesized to provide their hosts with nutrition by extracting organic compounds from the whale bones. We investigated the diversity and distribution of symbiotic bacteria in *Osedax mucofloris* from shallow-water whale-falls in the North Atlantic using comparative 16S rRNA sequence analysis and fluorescence in situ hybridization (FISH). We observed a much higher diversity of symbionts than previously found in deep-sea *Osedax* species. Symbiont sequences fell into eight phylogenetically distinct clusters (with 91.4 – 98.9% similarity between clusters) and considerable microheterogeneity within clusters (99.5 – 99.7% similarity) was observed. Statistical analyses of shallow versus deep-sea *Osedax* symbionts revealed a highly significant effect of the host species and whale fall depth on symbiont diversity and distribution. Within the *O. mucofloris* population, statistical analyses revealed a highly significant effect of the host individual on symbiont diversity and distribution, with 70% of the variability between clusters and 40% of the variability within clusters explained by this effect. FISH analyses showed that most host individuals were dominated by symbionts from a single cluster, with symbionts from less abundant clusters generally confined to peripheral root tissues. Explanations for the observed diversity and distribution patterns include host specificity, whale fall depth, competition between symbionts for colonization of root tissues, and genetic variability of the free-living symbiont stage over time or space.

Observations of deep pelagic polychaete egg cases

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MBARI

The formation of egg cases by benthic polychaetes has been well documented, however, reproductive strategy has not been described for their pelagic relatives. Very little is known about the reproductive biology of the holopelagic Tomopteridae and Alciopidae, commonly found in all the world's oceans. Since 1988, The Monterey Bay Aquarium Research Institute has recorded over 16,000 hours of remotely operated vehicle (ROV) dive video from Monterey Bay and beyond. Using these ROV videos, we observed 133 pelagic polychaete egg cases at depths ranging from 50 to 1000 meters. These observations, although rare, occurred throughout the year, in all seasons. Most egg cases were composed of clear, spherical mucous surrounding many hundreds of larvae. Some egg cases appeared as bright green mucous. The egg cases ranged in size from a few centimeters to almost 50 cm in diameter. Using detritus samplers, special collection devices mounted on the ROVs, we collected undisturbed egg cases to confirm that they did, in fact, contain polychaete larvae; in some cases juvenile tomopterids were also found in the collections. We hope that future molecular analysis planned for these collected larval and juvenile worms will reveal their specific taxonomic

identity. This study represents the first description of the reproductive strategy employed by deep pelagic polychaetes. Continued observations of egg cases and adult polychaete behavior will provide insight into the reproductive biology of these common organisms, which may play an important role in the deep pelagic food web.

Novel ciliated larval form, unique brooding, and early release of vent gastropod *Ifremeria nautilei*

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Ifremeria nautilei is a large, symbiont-harboring gastropod found in the southwestern Pacific hydrothermal vent fields. *I. nautilei* is quite abundant, but its ontogenetic and larval development has not been revealed as in other provannid species which usually lack protoconchs. In this presentation, we will show a new egg-brooding feature and a new larval type discovered in *I. nautilei* from the hydrothermal vent fields in the Manus and North Fiji back-arc basins. *I. nautilei* have a special brooding pouch in their head-foot and release their larvae from a pore located in the center of the sole. The released larvae resemble trochophores, but have several distinct differences: they possess a unique external cuticle, a fully ciliated surface with no evidence of a prototroch derived from trochoblast cells, and asymmetrical features. We have identified this as a new larval form and have named it “Warén’s larvae”, in honor of Dr. Anders Warén. Warén’s larvae released from shipboard specimens developed into veliger larvae about a week after release from the parent under high temperatures (> 20°C). The discovery of this new larval type reflects the diversity of larval development in vent and other chemosynthetic environments. Its characteristic cilia, external cuticle, and early release may be linked to the dispersal potential of *I. nautilei*.

Atlantic - Pacific relationships of deep-sea octocorals

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During the period 2003-2005 a series of 34 dives were made on 13 seamounts in the New England and Corner Rise Seamount Groups, NW Atlantic Ocean. Octocorals, black corals, and a variety of associated invertebrates were collected. Identification of the octocorals has proceeded slowly because most of the species are new to science and not associated with the otherwise moderately well-known North Atlantic fauna. As species have been documented, using both morphological and molecular data, it has become apparent that for a number of

genera, the closest living relatives of several of the new North Atlantic species are to be found in the central and SW Pacific. Genera with sibling (geminate?) or similar species in the Atlantic and Pacific include *Paragorgia*, *Paramuricea*, *Chrysogorgia*, *Rhodaniridogorgia*, and *Iridogorgia*. Additional pairs have also been found in the Keratoisidinae, but the taxonomic work on that subfamily is not yet complete. We will examine the hypothesis that movement of North Atlantic Deep Water through the Central American Seaway as late as 11 mya, is the most likely explanation for these close relationships. The alternative hypothesis, that these species are ancient Tethyan hold-overs, will also be examined, but that the last possible date for Atlantic – Pacific connections through the Tethyan seaway is too long ago.

Feeding ecology of meso- and bathypelagic zooplankton as indicated by scanning electron microscopy of fecal pellets from live animals and sediment trap samples

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The characteristics of zooplankton fecal pellets are diagnostic of taxa and diet. Meso- and bathypelagic zooplankton are hypothesized to feed on sinking particles as well as other zooplankton but little is known about their feeding ecology. In this study, material collected in sediment traps moored at 3500 m (600 m above the bottom) at the abyssal time-series Station M, was analyzed for the contribution of zooplankton fecal pellets to particulate organic carbon (POC) flux. Intact fecal pellets isolated from the samples were observed using light and scanning electron microscopy (SEM) to determine if differences in pellet shape and color reflected the content of the pellets. We also collected several mesopelagic zooplankton species via remotely operated vehicles and midwater trawls in Monterey Bay and incubated them overnight to collect their fecal pellets. These pellets were then observed microscopically and compared to trap pellets. In the trap samples, the identifiable material in most pellets consisted of phytodetritus (e.g. diatoms, silicoflagellates, and coccolithophores) and radiolarian fragments, although the proportion of each varied by season and pellet type. The pellets of the mesopelagic copepod *Gaussia princeps* consisted predominately of phaeodarian radiolarian fragments, minipellets and phytodetritus. Ostracod pellets contained a mixture of crustacean fragments, phytodetritus, and unidentifiable material. The data generated from this study will further our understanding of the role of zooplankton in the food web of the deep-sea.

Zooplankton in the Eastern Tropical North Pacific oxygen minimum zone

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As part of the Eastern Tropical Pacific Project (ETP Project), we examined distributional and ecological responses of zooplankton to the strong vertical environmental gradients of the oxygen minimum zone (OMZ) in this region. Zooplankton were collected in vertically-stratified MOCNESS tows day and night to 1200 m during cruises in 2007 and 2008 at two stations along a north-south transect from 13° N to the Costa Rica Dome (9° N). Parameters measured included size-fractionated zooplankton biomass, copepod abundances and distributions, community structure of major taxa, and trophic webs. Highlights of the deeper

samples include (1) a narrow biomass peak at the lower OMZ oxycline, (2) zonation of communities associated with OMZ environmental structure and subzones, (3) temporal and spatial variation in deep resident layers of the copepod *Eucalanus inermis*, and (4) unusual trophic interactions. These data will contribute to assessing ecosystem effects of potential future expansion of OMZs as a result of global warming.

Climate change, pelagic-benthic coupling and deep-sea ecosystem functioning

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Deep-sea communities rely on POC produced in surface waters for food, and deep-sea benthic communities rapidly respond and process freshly deposited material, with both the quality and quantity of available organic matter (OM) exerting control on the rates and pathways of OM degradation. At the same time, deep-sea sediments are a major reservoir in the global carbon cycle and the cycling or burial of organic matter mediated by benthic communities are key terms in the global C, N and P cycles, linked to ocean nutrient budgets and productivity. POC flux into the deep-sea BBL is strongly correlated with regional climate indices, and, consequently, climate change-related changes in upper ocean conditions are likely to rapidly cascade down to the deep-sea floor and may trigger changes in the structure of deep-sea communities and the ecosystem services they perform. But our ability to predict the potential consequences of such changes is constrained by our limited knowledge of the susceptibility of most deep-sea organisms to such change. Macrofauna organisms can be ecosystem engineers that significantly alter the habitat structure, geochemical setting and food supply for other organisms, and the loss of such a keystone species could have profound impact on benthic communities. In this talk, results from macrofauna food choice experiments, carried out as in situ experiments with different, stable-isotope-labelled phytoplankton organisms, will be presented and potential consequences for benthic ecosystems discussed.

Effect of hydrostatic pressure on copepod's eggs

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In order to determine the pressure tolerance on copepod's eggs, the egg development times of five copepods, *Neocalanus cristatus*, *N. plumchurs*, *N. flemingeri*, *Calanus sinicus*, and *Acartia steueri*, and egg hatching successes of six copepods, *N. cristatus*, *N. plumchurs*, *N. flemingeri*, *C. sinicus*, *A. steueri*, and *Paracalanus parvus*, at four pressure conditions (i.e., 1, 10, 50, and 100 atm) and four temperature conditions (i.e., 10, 15, 20 and 25°C) were examined. The experiments of three *Neocalanus* species were conducted at only 4°C. Eggs of three *Neocalanus* species are released at deep layer from about 300 to more than 1000 m depth, while eggs of *C. sinicus*, *A. steueri*, and *P. parvus* are produced at shallow layer from 0 to a.c. 20 m depth. The egg development times of five copepods were similar to those at 1 atm, and this means these egg development times were not affected by the pressure conditions. Effects of hydrostatic pressure on egg hatching successes were different among the species. Egg hatching successes of *N. cristatus*, *N. plumchurs*, *N. flemingeri*, *A. steueri*, and *P. parvus* at the high pressure conditions were as high as those at 1 atm, while that of

C. sinicus was decreased with pressure increasing. Only eggs of *C. sinicus* did not have high pressure tolerance among shallower species. Egg pressure tolerance is not always related to vertical distribution and depth of laying eggs.

Temporal latitudinal-gradient dynamics and tropical instability of deep-sea species diversity for the last 500,000 years

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A benthic microfaunal (Ostracoda: Crustacea) sediment record from the equatorial Atlantic Ocean over the past four glacial-interglacial cycles was investigated to understand temporal dynamics of deep-sea latitudinal species diversity gradients. The results demonstrate unexpected instability and high amplitude fluctuations of species diversity in the tropical deep ocean that are correlated with orbital-scale oscillations in global climate. Species diversity is lowest during glacial and highest during interglacial periods. This implies that climate severely influences deep-sea diversity, even at tropical latitudes, and that deep-sea latitudinal species diversity gradients, while generally present for the last 36 million years, were weakened or absent during glacial periods. Temporally dynamic latitudinal species diversity gradients and unstable tropical diversity require reconsideration of current ecological hypotheses about the generation and maintenance of biodiversity as they apply to the deep sea, and underscore the potential vulnerability and conservation importance of tropical deep-sea ecosystems.

Megafaunal scavenger ecology of the California slope

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Baited cameras have offered much insight into the ecology of scavenging animals in many parts of the world's oceans, revealing patterns of vertical zonation, trends in size and abundance with depth, and aspects feeding behavior. It is surprising, then, that within this body of literature very little has been published on the scavenging community off of the California continental slope where work of this nature originated (Issacs and Schwartzlose 1975). Here we present a study of megafaunal scavenger ecology encompassing a wide range of taxa from shelf to abyssal depths off of the central Californian coast. Thirteen deployments from 100 – 3000 m of a baited time-lapse free-vehicle camera system photographed 26 taxa attracted to bait. In contrast to other baited-camera studies, decapod crabs represented a large portion of the scavenging assemblage (31% of all species) while Synphobranchid eels, a cosmopolitan scavenging group found almost ubiquitously in world's oceans, were not observed at all. Relative scavenger abundance (measured as N_{max} - peak number of individuals in the field of view) showed no trend with depth while species richness displayed a parabolic trend with depth, peaking at 9 species at 2000 m. The inverse square model – a widely published model estimating fish density based on first arrival times of fish to bait – was applied to *Antimora microlepis* and *Coryphaenoides armatus* and compared to trawl data gathered from the same cruise, yielding no significant correlation between the two estimates. During one deployment at 3000 m, *C. armatus* was used as bait, resulting in a complete

absence of *C. armatus* compared to Nmaxs of 10 and 12 individuals observed at similar depths and locations using non-macrourid bait. This observation further supports the hypothesis that macrourid fishes actively avoid areas where dead or dying conspecifics are present.

Does ecological release from predators permit slow development and extended planktonic periods in deep-sea embryos and larvae?

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Embryos and larvae of deep-sea animals show consistently slower cell cycles and longer planktonic periods than comparable stages of related shallow-water species, including ones that develop at similar temperatures. Because this phenomenon is seen in both bathyal and abyssal species, it is unlikely to be a physiological response to pressure. In shallow water, cell cycles tend to be longer in encapsulated and brooded embryos than in freely-spawned planktonic embryos. This difference has been attributed to the dangers of planktonic development, including predators. We have recently reared the larvae of two bathyal cidaroid echinoids to metamorphosis, the first deep-sea echinoderms for which we know the full and actual duration of the planktonic period. Both species have long cell cycles in early development and extremely long pelagic lives compared to related echinoids from shallow water. Cell cycles of other deep-sea echinoderms are also significantly longer than those of their shallow counterparts, and limited information on polychaete, mollusk and ascidian development suggests similar patterns. We speculate that lower densities of micropredators permit the evolution of slower developmental rates and longer planktonic periods in the deep sea. Food limitation may also select for long planktonic periods in species with planktotrophic larvae.

Abstracts of Poster Presentations

Molecular genetic characterization of *Desmophyllum dianthus* (Anthozoa, Hexacorallia) from the Mediterranean Sea: a preliminary study

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Desmophyllum dianthus (Esper, 1794) is an azooxanthellate scleractinian coral widely distributed in the ocean in a depth range comprised between 8-2500 m. *D. dianthus* is currently classified in the family Caryophylliidae on the basis of skeletal morphology. Caryophylliidae is not convincingly characterized by well defined morphological characters and available molecular data are somewhat equivocal (Romano and Cairns, 2000).

In the Atlantic ocean and Mediterranean Sea *Desmophyllum dianthus* typically occurs at bathyal depths often associated with framework building species such as *Lophelia pertusa* and *Madrepora oculata*. In spite of its relative abundance in geographically disconnected coral stocks throughout its range, virtually no comprehensive molecular information is available on this taxon. Living specimens have been then collected from several sites of Mediterranean Sea at depths of c. 300 - 500 m in order to carry out their genetic characterization. The main scope of this research aims at clarifying the phylogenetic relationships of *Desmophyllum dianthus* and, above all, the structure and divergence within and among Mediterranean populations based on molecular analyses of ITS and 28S encoding genes. Our initial results seem to document only a slight genetic difference between corals specimens, perhaps suggesting the case of slow evolution for this species but also calling for further in-depth genetic investigation based upon new markers.

Genetic Paternity test of *Cephalurus cephalus*, lollipop catshark (Scyliorhinidae), by random amplified polymorphic DNA techniques

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Cephalurus cephalus (Gilbert, 1892) is a bathydemersal species found in the tropical eastern Pacific from Baja California to northern Chile. Lollipop catshark is an aplacental viviparous or ovoviviparous species. On 11 February 2007, during the launch of the TALUD project, a total of 18 *C. cephalus* were caught (13 embryos and 5 adults) at depths between 464 to 486 m in the Gulf of California (TALUD X, St. 12, 28°01'36 N; 111°51'50"W). Total length (LT, mm) were recorded. Because there is a possibility that embryos has been aborted for one of

the two mature females cached in the same haul, the random amplified polymorphic DNA (RAPD) assay was used to test paternity. Almost the same band pattern were recorded for all 13 neonates (genetic similarity > 95%), and between them and female F1 (243 mm LT) genetic similarity were >92%. results could have different interpretations. For example: If Female F2 is a rare genotype ($p=0.001$) and F1 is a common genotype ($p=0.99$) then the fact that the neonates have a similar genotype to the female F1 is not especially significant (Case 1). However, if it is the other way around such that F1 is the rare genotype ($p=0.001$) and F2 the common genotype ($p=0.99$), then the fact that the neonates have the same genotype as the F1 female would likely be very significant (Case 2). If Case 2 is true, then 13 embryos are brothers and sons of F1 female.

New depth record of *Coryphaenoides capito* (Garman, 1899) Bighead grenadier (Gadiformes: Macrouridae) from the Gulf of California, Mexico

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Coryphaenoides capito (Garman, 1899) is a bathypelagic species found in the tropical eastern Pacific from Baja California to northern Chile. The Bighead grenadier is found at depths between 305 and 1000 m (Iwamoto, y Schneider, 1995). Data came from seven survey hauls. Specimens were collected aboard the R/V “El Puma” of the Universidad Nacional Autonoma de Mexico. *C. capito* was collected on 13 of 78 trawls. Deep range of 7 stations was 750 to 966 m (strata 1000 m) and for the other 6 was 1097 to 1750 m (strata 1001 m). Differences in size structure were tested between those deep strata. A multinomial distribution was used to estimate the size-composition by analyzing the total-length frequencies. A total of 41 organisms were recorder, 18 into the strata 1001 m and 23 into the strata 1001 m. In total, 3 modal groups (G1, G2 ad G3) were detected, the means \pm standard deviations of modal groups were 15.6 ± 1.4 mm ($n=13$) for G1, 20.5 ± 1.2 mm ($n=13$) for G2 and 24.5 ± 1.4 mm ($n=13$) for G3, respectively. All groups were found in both strata; specimens of G1 were more abundant in strata 1000 m, whereas, specimens of G2 and G3 were more abundant in strata 1001. This seems to indicate that bigger organisms show a tendency to inhabit deeper places than smaller ones.. Twenty-three Bighead grenadiers were collected deeper than 1000 m, until now, the presence of *C. capito* below 1000 m has not been reported in the literature (Iwamoto and Schneider, 1995). One specimen was caught on 25 August 2000 (TALUD VII, St. 20) at a depth of 1750 m. This new record extends the known deeper range of occurrence approximately 750 m deeper than the previously reported limit. Keywords: Gulf of California, new record; maximum depth, Macruridae.

***Dibranchius spinosus* (Garman, 1899) distribution in the Mexican central Pacific**

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The batfish *Dibranchius spinosus* (Garman, 1899) is a bathydemersal species found in the oriental Pacific, from Baja California to Peru its depth range is from 605 to 1400 m (Bradbury, 1999). *D. spinosus* was one of the most abundant species in the TALUD Project and was collected on 25 of 116 trawls. Data came from ten survey hauls. Specimens were collected aboard the R/V “El Puma” of the Universidad Nacional Autónoma de México. The sampling device, a 2.35 m wide, 0.90 m high epibenthic sledge equipped with a collecting net of about 5.5 cm stretched mesh size, was operated at depths of 750 to 1750 m. The objective is to provide information of the size structure and distribution patterns of *D. spinosus* in the south center Gulf of California and the Mexican central Pacific. A multinomial distribution was used to estimate the size-composition by analyzing the total-length frequencies. The LT range was 3.8 to 18.3 cm. Three organisms (17.5, 17.5 y 18.3 cm) were bigger than the maximum reported size (Bradbury, 1999). The size structures reveal the presence of 3 modal groups; G1 with 3 organisms smaller than 5 cm, G2 with 42 organisms ($6 \leq LT \leq 13$ cm) and G3 with 18 organisms ($12 \leq LT \leq 18.3$ cm). About depth, G1 was only captured at the bathymetric range of 815 and 870 m. Most of the organisms of G2 and G3 were distributed at the 700 and 1300 m range. There is no evidence of size variation with depth. In the present study were reported 4 organisms captured between 1526 and 1750 m. This new bathymetric record increased 311 m the previous reported by Bradbury (1999). Keywords: Mexican central Pacific, Gulf of California, new record; maximum depth, Ogcocephalidae.

Bathymetric and latitudinal gradients in the diversity of pelagic ostracods in the Central Eastern Atlantic Ocean

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Pelagic ostracods are an ecologically important but little-known component of the marine holozooplankton. They are numerically abundant in oceanic regions and throughout the water column, often numerically ranking second after the Copepoda. Planktonic ostracods were identified from samples collected in November 2007 during R/V Polarstern cruise ANT-XXIV in the eastern Atlantic Ocean under the aegis of the Census of Marine Zooplankton (CMarZ). Zooplankton was collected from four stations ranging from 11°N to 25°S from the surface to a depth of 1000 m using a MOC-1 and from 1000-5000 m using a MOC-10 net system. Both samplers were fitted with 0.32 mm mesh. CMarZ has focused on under-sampled regions of the world oceans, including the deep mesopelagic and abyssopelagic ocean realms. The aim of this specific project is to assess the species composition and richness of the pelagic Ostracoda. More than 22,500 specimens were sorted at sea, which included at least 98 species. More than six species from the total number of collected ostracods are either novel or are awaiting description. Preliminary comparison of the species composition sampled at each

station, revealed large latitudinal changes. In the upper 1000 m the species are mostly well known and changes in faunal composition appeared to be related either to changes in the water masses, or to latitudinal shifts in the seasonality of the production cycle and hence organic fluxes. Novel species were collected at the abyssopelagic depths and these samples included many ostracods species that have rarely been caught before. Several of these deep living species appear to be distributed ubiquitously throughout the deep ocean.

The Census of Marine Life ChEss Programme - global puzzle of deep-water chemosynthetic ecosystems: 8 years of discovery and investigation

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ChEss is a project within the Census of Marine Life initiative. Since the onset of this project in 2002, an international group of ChEss scientists have been collaborating to address the issues of biogeography and biodiversity of deep-water chemosynthetic ecosystems and to understand the processes driving them. As a result of numerous ChEss-hosted meetings and workshops, extensive fieldwork and laboratory investigations have been conducted around the globe to discover and explore new chemosynthetic sites at key locations. This poster displays some of the highlights of the ChEss programme.

Small (≤ 10 km) spatial-scale variability in the distribution and biodiversity patterns of deep macrobenthic communities along the North-west Sardinia lobe: preliminary results

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The comprehension of spatial scale patterns of distribution, abundance and biodiversity of the deep-sea benthic communities has always been a challenge. Our recent studies on deep-sea macrofaunal communities on large (>100 km) spatial scale in the central-eastern Mediterranean Sea, appear to confirm a sharp decrease in the benthic organism, both in abundance and biomass, with increasing depth and from West to East. Abundance and biomass values ranged from 610 ± 362 ind/m² (1238 m, central Med) to 31 ± 20 ind/m² (2752 m, eastern Med), and from 0.77 ± 0.56 g/m² (1238 m, central Med) to 0.02 ± 0.01 g/m² (2700 m, eastern Med) respectively. It is accepted that a decrease in the nutrients input to the deep-sea floor is a likely reason for this decline. In this study we focus on the role of food and sediment type vs. depth in shaping distribution and biodiversity variability of the deep-sea macrobenthos at the smaller (≤ 10 km) spatial scale. Macrobenthic community variability at this scale is in fact not known, yet essential to postulate a gradient with depth or longitude.

Specific aims of this study are: i) to characterize the distribution, abundance, biomass and diversity of deep-sea macrobenthos, both along bathymetric and horizontal transects; ii) to explore the importance of food availability and sediment granulometry in influencing macrofaunal communities at the small spatial scale; iii) to quantify how our variables contribute to shaping macrobenthic communities along spatial gradients. To achieve these aims, on October 2009 a total of 96 box-corer deployments were performed along a slope area off NW Sardinia (Mediterranean Sea), from the continental shelf break to the bathyal plain. Four box core replicates were collected at each of 8 increasing depths, from 300 to 2400 m, every 300 m. The measurements were made along three parallel transects, ~1 km apart . In here we present our preliminary results.

Diversity, dispersal and succession of whale-fall fauna in the deep sea

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Habitat heterogeneity in the deep sea contributes significantly to nematode diversity, yet meiofaunal assemblages at chemosynthetic habitats have been understudied owing to limited sampling effort and available species-level data. Recently it has been found that at both hydrothermal vents and cold seeps nematode diversity is low, that dominance is high and that even over significant distances nematode species and genera assemblages are similar (Flint et al 2006; Zekely et al 2006; Copley et al 2007; Gollner et al 2007). Similarly, macrofaunal assemblages are similar between widely distributed chemosynthetic habitats, including whale carcasses (Smith & Baco 1998; Dahlgren et al 2004) and clear phylogenetic relationships have been found within taxa occurring at a number of chemosynthetic habitats types; molluscs and polychaetes for example (Distel et al 2000; Glover et al 2005). Consequently, it has been postulated that deposited whale-fall carcasses represent habitat islands on the sea floor, intermediate between chemosynthetic environments, and that they have significant evolutionary and ecological importance with regard to dispersal and speciation (Smith et al 2002; Glover et al 2005). New data presented here, however, suggests that nematode assemblages at whale fall sites may not be similar to those recorded at hydrothermal vents or seeps – genera shown to particularly characterise these habitats not being present or present in low numbers. Equally, although the nematode fauna was diverse, with high rates of species turnover identified as the carcass degraded, common deep sea genera such as *Acantholaimus* and *Halalaimus* were also relatively under-represented.

Patterns of distribution of deepwater demersal fishes of the North Atlantic mid-ocean ridge, continental slopes, islands and seamounts

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Spatial and bathymetric distribution of deepwater benthic and benthopelagic fishes from the North Atlantic continental margin, oceanic islands and seamounts, and the Mid-Atlantic Ridge was analysed with the aim to reveal spatial and depth-related patterns at a basin-wide scale. Depth-stratified presence-absence data for 610 species were compiled from fisheries-independent trawl studies with full species lists. The datasets comprised trawls conducted on the upper continental slope (200 m) to abyssal depths, and 750 m wide depth strata were used. Number of species and families decline with depth in all areas. Species number is highest in the Western North Atlantic, significantly lower on the Mid-Atlantic Ridge and Eastern North Atlantic. It is suggested that species numbers are low in southern areas (Bahamas, NW Africa, southerly seamounts), but the sampling effort in these waters has been much lower than in northern sites. Fish assemblages vary by depth, latitude and longitude and the study corroborates earlier suggestions that assemblages are broadly distributed in relation to regional circulation and watermass features. The Mid-Atlantic Ridge assemblages between Iceland and the Azores are similar to those on Eastern North Atlantic slopes and rises, but dissimilar to all others, including Western Atlantic, Greenland, northwest African, and Azorean seamount and island assemblages. Across the North Atlantic differences between sub-areas are strongest at slope depths, much less pronounced at the less speciose rise and abyssal depths.

Community structure in sediments around kelp and wood falls in the deep NE Pacific and species overlap with other reducing habitats

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Sunken parcels of macroalgae and wood provide important oases of organic enrichment at the deep-sea floor, yet sediment community structure and succession around these habitat islands are poorly evaluated. We experimentally implanted 100 kg kelp falls and 200 kg wood falls at 1670 m depth in the Santa Cruz Basin to investigate (1) macrofaunal succession, and (2) species overlap with nearby whale-fall and cold-seep communities over time scales of 0.25 to 5.5 y. The abundance of infaunal macrobenthos was highly elevated after 0.25 and 0.5 y near kelp parcels with decreased macrofaunal diversity and evenness within 0.5 meters of the falls.

Apparently opportunistic species (e.g., two new species of cumaceans) and sulfide tolerant microbial grazers (dorvilleid polychaetes) abounded after 0.25 - 0.5 y. At wood falls, opportunistic cumaceans become abundant after 0.5 y, but sulfide tolerant species only became abundant after 1.8 - 5.5 y, in accordance with the much slower buildup of porewater sulfides at wood parcels compared to kelp falls. Species diversity decreased significantly over time in sediments adjacent to the wood parcels, most likely due to stress resulting from intense organic loading of nearby sediments (up to 20-30% organic carbon). Dorvilleid and ampharetid polychaetes were among the top-ranked fauna at wood parcels after 3.0 - 5.5 y. Sediments around kelp and wood parcels provided low-intensity reducing conditions that sustain a limited chemoautotrophically-based fauna. As a result, macrobenthic species overlap among kelp, wood, and other chemosynthetic habitats in the deep NE Pacific are primarily restricted to apparently sulfide tolerant species such as dorvilleid polychaetes, opportunistic cumaceans, and juvenile stages of chemosymbiont containing vesicomylid bivalves. We conclude that organically enriched sediments around wood falls may provide important habitat islands for the persistence and evolution of species dependent on organic- and sulfide-rich conditions at the deep-sea floor and contribute to β and γ diversity in deep-sea ecosystems.

Community structure of infaunal macrobenthos around vestimentiferan thickets at the San Clemente cold seep, NE Pacific

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The San Clemente cold seep lies within 100-200 km of other reducing habitats in the NE Pacific, offering an opportunity to compare diversity and species overlap among reducing habitats (i.e., whale, kelp, and wood falls) at similar depths within a single region. Video observations from the research submersible *Alvin* at the San Clemente seep (1800 m depth) indicated clumps (“thickets”) of vestimentiferans distributed as meter-scale patches interspersed with vesicomylid clam beds and black sediments. Sediment-core samples were collected at distances of 0 to 80-200 m along randomly oriented transects radiating outward from vestimentiferan thickets to evaluate changes in macrofaunal community structure from thickets into the background community. Macrofaunal abundance was elevated at distances of 0 - 1 m compared to 80 - 200 m (i.e., the “background” community). The tube-building frenulate worms *Siboglinum* spp., along with peracarid crustaceans, dominated sediments within 1 m of vestimentiferan thickets. Species diversity was depressed within 1 m of thickets but with high rates of species accumulation, suggesting that seep sites greatly increase sediment heterogeneity and facilitate colonization by non-background macrofaunal species. Stable isotope data indicate chemosynthetic nutrition for a few dominant macrofaunal organisms within 1 m of tubeworm thickets. The macrofaunal community near vestimentiferan thickets in San Clemente seep contains intermediate levels of species richness and diversity compared to other deep-sea seep areas in the northeast Pacific. There was low species overlap between San Clemente seep macrofauna and communities in reducing habitats near wood-, whale- and kelp-falls at similar depths within the region, suggesting that seeps harbor a distinct infaunal community.

Denitrification: not just for prokaryotes anymore?

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Until recently, the process of denitrification (conversion of nitrate or nitrite to nitrous oxide and/or nitrogen gas) was thought to be performed exclusively by prokaryotes and some fungi. Recent work suggests complete denitrification in certain foraminifera inhabiting micro-oxic environments. This important finding impacts our understanding of nitrogen losses from the marine environment as well as fundamental concepts of eukaryotic respiration. However, details of this process and the sub-cellular location of these reactions in foraminifera remain unclear. For example, endobionts, rather than the foraminifer proper, could be performing denitrification in some cases. Here we measured intracellular nitrate concentrations and nitrogen isotope ratios ($\delta^{15}\text{N}$ of nitrate) in several species of benthic foraminifera recovered from Santa Barbara Basin. Where measurable, intracellular nitrate had elevated $\delta^{15}\text{N}$ values, suggestive of nitrate consumption within the foraminifera. We also detected genes *nirS* and *nirK*, which encode two different forms of dissimilatory nitrite reductase involved in denitrification, in DNA extracted from foraminifera. While we originally hypothesized that *Bolivina argentea*, which lacks endobionts and sequestered plastids, would be unable to denitrify, the gene *nirK* was detected in *B. argentea* DNA. In addition, suboxic and anoxic incubations of *B. argentea* from laboratory maintenance cultures revealed a decrease in intracellular nitrate concentration and increase in $\delta^{15}\text{N}\text{-NO}_3^-$ over time, which is indicative of nitrate respiration, or denitrification. Further results suggest that denitrification occurs in a range of foraminiferal species, including some lacking endobionts and some possessing endobionts (including some chloroplast-husbanding species), implying that microbial associates are not solely responsible for this process in foraminifera.

On some meiofauna from the Galician continental slope obtained during the campaign DIVA-Artabria 2009 on board R/V Sarmiento de Gamboa

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During October 2009, we undertook an oceanographic expedition on board of the Spanish vessel R/V Sarmiento de Gamboa. We mainly worked on the bottoms of the Galician Bank and the abyssal plain collecting some samples from the continental slope. The sediment was obtained with a box-corer grab and each corer was divided into three samples, two of them for the study of the meiofauna and the third one for the assessment of the sedimentological parameters. Each sample was sliced into some subsamples with a height of 1 cm showing the following depths in the sediment: 8 cm (Stn. 93), 20 cm (Stn. 94) and 5 and 7 cm (Stn. 95). The depth of the different stations was 260 m (Stn. 94), 261 m (Stn. 93) and 264 m (Stn. 95)

respectively. The subsamples were fixed with ethanol 70% and later washed up in the laboratory with a megafuge using kaolin and ludox as dispersant agents, and sieved using a mesh of 30 µm in size. The meiofauna was hand-sorted manually, under a stereomicroscope. In the present poster we display the preliminary results about the meiofauna, showing both the total and vertical distribution in each sediment sample.

Diversity of Tanaidacea (Crustacea) of European mud volcanoes

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While exploration of the unusual and diverse faunas associated with deep-sea mud-volcanoes have been increasing over the last few decades, the smaller macrofaunal taxa are only recently receiving detailed study. Tanaidaceans are a group of peracarid crustaceans which are numerous and diverse in the deep seas, to the point of being dominant in certain areas, yet there have been only four published studies to date of the tanaidaceans at mud volcanoes, revealing a number of unique species and apparently endemic genera. In an ongoing investigation of the fauna from mud-volcanoes in the Gulf of Cadiz, a total of over one thousand specimens of tanaidacean were collected, representing over 80 distinct putative taxa. As a number of these taxa appear to be vent-associated endemics, the present study has investigated taxonomic relationships between the remarkably diverse tanaidacean assemblages at four disparate deep-sea mud-volcano sites around the north Atlantic and Mediterranean, which may shed some light on the evolution, rates of zoogeographic spread or isolation, endemism and allopatric speciation of these taxa. These relationships suggest that age of the sites and their geological association via plate tectonics offer the best interpretation, with implications for the age of the isolation and subsequent speciation of closely-related taxa.

First evidence of parasitic behaviour in deep sea *Exspina typica* (Crustacea: Tanaidacea)

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The order Tanaidacea includes more than a thousand species, which are mainly free living or tube-dwelling detritivores, followed by grazers or filter feeders. *Exspina typica* (Lang, 1968) represents the unique exception to these common life styles, having being found in the intestine and body cavity of different deep sea holothuroid species. This species has a very broad distribution, having been recorded in Kermadec Trench, Kurile-Kamchakta Trench,

New Zealand, Porcupine Abyssal Plain, the Caribbean as well as in the Southern Ocean, ranging from 385 to 4950 m. Thurston et al. (1987) was the first to confirm the association with deep water holothuroids, as the unique previous record (Sieg, 1979) has been considered doubtful, since the host examined was eviscerated and in a bad shape. *E. typica* does not show any clear adaptation to a parasitic life style, although the reduction of mandibular molar and setation in maxillulae might be due to this life style. So far, this partnership has never been defined as regard as the mutual relations occurring between the two partners. Thanks to the samples collected in the framework of the IPY-CAML Cruise of the R/V Tangaroa (NIWA, Wellington, NZ), held in the Ross Sea in 2008, it has been possible to define this association as a parasitic one. In fact, several specimens of *E. typica* were found inside the holothuroid *Scotoplanes globosa* Théel, 1882 . These specimens have been documented to live inside the coelomatic cavity of the host and also to actively ‘dig’ in its skin, producing ‘corridors’ in the body wall of the host by grasping its tissue with the claw. This association, which is herein reported for the first time for Antarctica, has to be considered a truly parasitic one. Apparently, only the females of *E. typica* have been documented to live in associations with holothurians, suggesting a relationship with the reproductive cycle of the tanaid species.

The role of deep water zooplankters in feeding ecology of Little Auk – the matter of quality

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Although little auk (*Alle alle*) is the most numerous planktivorous sea bird of Svalbard archipelago, the full spectrum of its zooplankton prey is still unknown. Recent studies carried out in Svalbard colonies showed that despite little auk’s limited ability to dive only to the depth of about 35 m, some deep-water organisms (e.g. copepod *Paraeuchaeta* spp., euphausiid *Thysanoessa longicaudata*, squid *Gonatus* sp. and fish *Sebastes* sp.) are regularly found in the food brought by adult birds to the colonies to feed their chicks. However, data from zooplankton sampling indicates that the juvenile stages of these deep-water inhabitants are found in the upper water layers in much lower concentrations in comparison to more common epipelagic zooplankters (e.g. *Calanus finmarchicus* and *C. glacialis*). Most of the deep-water invertebrates accumulate high energy lipids with long chained fatty acids. They biosynthesize these lipids mainly before achieving the adult stage, thus juvenile forms (available for the diving little auks) could be a source of profitable food for the birds, that is rich in energy and important substances (long chained fatty acids). To estimate the role of the juvenile stages of deep-water zooplankters and nekton organisms in feeding ecology of the planktivorous birds, we present the results of studies on food composition of little auk carried out in 2007-2009 in two Svalbard (European Arctic) little auk colonies: Magdalenefjorden (79°35' N; 11°05' E) and Hornsund (77°00' N; 15°31' E). The results of our study point to the importance of so far unexplored and remarkable energy pathways in the relatively short Arctic food webs.

Phylogeny of the deep-sea protobranch subfamily, Ledellinae

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The mechanisms responsible for the origins of the diverse deep-sea benthos are not well known, and their evolutionary history is poorly resolved. This is especially true for the protobranch bivalves, which are more common in deep-sea habitats than in shallow water. We use geographically and bathymetrically referenced phylogenies to test hypotheses about the evolution of the endemic deep-sea protobranch bivalve subfamily Ledellinae (Family Nuculanidae). DNA from species in the genera *Ledella*, *Spinula*, *Bathyspinula*, and *Tindariopsis* was amplified from formalin-fixed ethanol preserved (FFEP), dried museum, frozen, and ethanol-preserved samples. The mitochondrial 16S and the nuclear 18S genes were amplified and sequenced using family and protobranch specific primers. Maximum likelihood and Bayesian phylogenies indicate that the subfamily is monophyletic, but within the subfamily, genera are not. Phylogenetic relationships inferred from 16S and combined 18S and 16S data show some differences but are generally congruent. Some clades within the subfamily contain species from the Atlantic, Southern and Pacific Oceans, suggesting multiple colonization events among the oceans. The abyssal cosmopolitan species *Ledella ultima* appears to be one of the basal species in the subfamily, suggesting that most species in the genus *Ledella* evolved from deeper species. Some abyssal *Spinula* and *Bathyspinula* species are basal as well. We also discovered mitochondrial heteroplasmy in at least two species in the Ledellinae. This is the first record of heteroplasmy within the protobranchs and represents the most basal bivalve taxon with heteroplasmy.

Geographic evidence for source-sink dynamics in deep-sea gastropods: an approach using nested analysis

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Recent evidence shows that the abyssal gastropod fauna of the North Atlantic is mostly composed of highly attenuated range extensions of bathyal species with larval dispersal ability. This suggests that many abyssal populations are sinks that experience chronic local extinction from vulnerabilities to Allee effects, and are maintained by continued immigration from more abundant bathyal source populations. This can be tested by performing a nested analysis to determine whether abyssal assemblages are statistically significant subsets of bathyal communities. A comparison of packed species presence-and-absence matrices to randomized null models shows that the actual distributional data are significantly structured. The rank order of nestedness among sites is highly correlated with depth indicating that progressively nested subsets occur in the predicted direction, toward the abyss. The nested pattern appears to extend downslope from mid-bathyal depths at around 2000 m. Where

reasonably accurate data are available, the nested rank order of sites is negatively correlated with animal abundance, and positively correlated with the proportion of species with larval dispersal ability as predicted by the presumed drivers of source-sink dynamics in this system. A comparison of the performance of eight nested metrics and six different null model algorithms suggests that the pattern of nestedness from the bathyal zone to the abyss is robust. Low abyssal endemism in gastropods implies that biodiversity is concentrated on continental margins.

DNA barcoding deep-sea Isopoda

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DNA barcoding for taxonomic routine identification promises to be an important tool in taxonomy and biodiversity research. Even though DNA barcoding is widely applicable, it is no stand-alone method or even a substitute for classical morphological taxonomy. The deep sea harbours great number of unknowns (> 80%). Many species remain undescribed and can be only superficially recognized for biogeographical and ecological studies. Providing such uncertainties in morphology, asellote isopods seem to be a good model taxon to infer applicability of molecular techniques in deep-sea isopod taxonomy. During DIVA-2 and ANDEEP-SYSTCO total DNA was extracted from muscle tissue using the Qiagen DNeasy Mini Kit applying an adapted version of the standard tissue protocol (~300 isopod specimens). Extracts were kept at -20 to -30°C. During ANDEEP-SYSTCO and DIVA-3 several hundred isopod specimens were dissected and several 96 well plates (barcoding racks) were filled with tissue. Lab work has been accomplished at Laboratories for Analytical Biology, Smithsonian NMNH, Washington, D.C.; USA in cooperation with the Barcode of Life Project in February and October 2009. For about 900 specimens, sampled during the recent expedition DIVA-3, belonging to 14 families, COI and 16S have been sequenced with a success of ~50% and ~80% respectively. For about 200 specimens belonging to the isopod families Dendrotonidae, Desmosomatidae, Echinothambematidae, Haploniscidae, Ischnomesidae, Mesosignidae, Munnopsidae, Nannoniscidae, Paramunnidae, Thambematidae, and the genus *Xostylus* (insertae sedis), six DNA markers (COI, 16S, 12S, 18S, 28SD1–3, 28SD6–8) have been sequenced recently (success ranges from 50–80%).

Biomass and metabolic partitioning amongst eukaryotic infauna from the bathyal deep-sea

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MBARI

Deep-sea infauna are important players in a plethora of globally important biogeochemical processes that occur at the deep-sea sediment/water interface. Marine eukaryotic infauna are typically separated into three faunal classes on the basis of size: macro-, meio- and micro/nanofauna. The smallest of these size classes, the micro/nanofauna (<32 µm and mostly protistan), are rarely quantified or considered in ecological models of deep-sea benthic processes. We have performed a comprehensive estimate of the biomass of all three size classes in a sediment community at 3100 m off central California, using microscopy and size to volume to carbon relationships. Based on these carbon estimates we calculated metabolic activity using allometric relationships. Total biomass was estimated to be 441 mg C m² composed primarily (71.5%) by macrofauna, followed by meiofauna (20%) and only 8.5% comprised of the smallest fraction. Estimates of metabolic activity were the inverse of the biomass segregation with micro/nanofauna comprising 62.4% of the total faunal activity followed by meio- and macrofauna at 19% and 18.6%, respectively. Although we have not conducted a similar comprehensive examination of 3 faunal fractions at other sites and depths we have analysed the micro- and nanofaunal classes at several sites with results consistent with the patterns mentioned above. Our results indicate that although the micro/nanofauna assemblages are typically low in biomass, they nonetheless play an important role in the function of deep-sea sediment assemblages and should be included in future deep-sea studies.

Revision of the deep-sea polychaete genus *Leptoecia* (Onuphidae) with description of a new species from the Mid-Atlantic Ridge

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Leptoecia (Onuphidae), a predominantly deep-sea genus of polychaetes, comprises six valid species inhabiting Antarctic, Pacific and North-Atlantic waters. Most of these species are known from a low number of specimens. More than 200 specimens of a new *Leptoecia* species have been collected at depths around 2600 m during the ECOMAR Cruise onboard the RRS James Cook to the Charlie Gibbs Fracture Zone area on the Mid-Atlantic Ridge in August–September 2009. *Leptoecia* sp. nov. differs from its congeners in having both uni- and bidentate simple anterior falcigers. Intraspecific variability of several diagnostic morphological characters (the shape of prostomium, dentition of anterior falcigers, the number of chaetiger of subacicular hooks origin, and the number of cirriform postchaetal lobes) was extraordinarily high compared to usual range of variability in other onuphids. A 473-bp 16S rDNA fragment was successfully obtained from seven individuals of *Leptoecia*

sp. nov. In two specimens a base alteration at the position 309 was found and in one of these specimens a base alteration at the position 156 also occurred. The low percentage of nucleotides divergence of the 16S rDNA gene confirmed that all analyzed specimens belong to the same species. Phylogenetic reconstruction of the genus *Leptoecia* based on the analysis of 13 morphological characters coded for seven *Leptoecia* species and two outgroups (*Hyalinoecia tubicola* and *Hyalospinifera spinosa*) yielded a single most parsimonious tree with 21 steps. Two major clades supported by exclusive synapomorphies could be recognized. The first clade contained two West Pacific species and the second clade included species from the North Atlantic, Antarctic and the East Pacific.

Characterisation of deep-sea habitats and biotopes within the MAREANO mapping area (Norwegian Sea/Barents Sea)

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The Norwegian seabed mapping programme, MAREANO covers benthic habitats down to 2700 metres in the northern Norwegian Sea and the southwestern Barents Sea. It is challenging and time-consuming to sample and observe the seabed at such depths. Thus, it is not possible to produce maps of habitats and biotopes, at a scale that matches the details provided by multibeam echosounder, based on seabed observation and sampling only. Therefore, one central activity in MAREANO is to find patterns of community distribution that can be related to environmental variables, or predictors with a full-areal coverage. Prediction of biotopes at a 200-meter scale has proven highly successful with around 85 % fit with test data sets for bank areas. The faunal composition on the slope is mainly correlated with depth, which is an expression of the pronounced environmental differences associated with the three major water masses in the area. Within these water mass “regions” acoustic backscatter is the second most important “community predictor”. This is a proxy for substratum type. Additionally, certain terrain descriptors (slope angle, rugosity, curvature, etc.) explains parts of the faunistic variation not explained by depth and backscatter in multivariate analyses. Four main habitats were identified: 1) upper slope, 2) lower rough (canyonized) slope, 3) lower smooth slope, and 4) the abyssal plain. The upper slope (from the shelf break down to ca 700 m) had the highest species diversity and the coarsest sediments, whereas the abyssal plain had lowest diversity and finer sediments. Here, we present results of analyses of observations recorded in the field as well as initial results from detailed analysis of video records. Environmental and faunistic characteristics for several biotopes found within these deep-sea habitats are described.

Distribution of cold-water corals around the UK and Ireland

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There are more cold-water coral records for the North Atlantic than any other area in the world, reflecting both its long history of deep-sea research and an increased focus on surveys of cold-water coral habitats over the past two decades. Some reports remain unpublished, thus we analysed available data on scleractinian, antipatharian, gorgonian and stylasterid coral distributions from benthic sampling expeditions from 1868-2008 around the UK and Ireland between 46-63°N out to 25°W, which include approximately 1500 records of deep-water corals (<200 m) including 29 scleractinian spp., 32 gorgonian spp., 10 antipatharian spp. and 6 stylasterid species. We show that, 65% of all cold-water coral records around the UK and Ireland are scleractinians. *Lophelia pertusa* is the most commonly recorded species of scleractinian. Gorgonians are the most species-rich order. Approximately 15 % of cold-water coral records around the UK and Ireland remain unidentified. Around the UK and Ireland, oil and gas exploration, pollution, bioprospecting, climate change and ocean acidification have all been highlighted as major concerns for marine conservation. Fishing, in particular, bottom trawling has had the greatest documented impact on cold-water corals, which has led to increased conservation efforts and a developing network of areas that are closed to demersal fishing gear along the continental shelf-break. Some of these protected areas are up for review in 2010, hence assessments need to be carried out as to whether existing management is effective. We present an overview of local advances in cold-water coral management starting with closure of the Darwin Mounds in 2004 followed by High Seas, UK and Irish closures in 2007-2008 and prospective changes as the current UK offshore SAC consultation moves forward. We give a bathymetric overview of all the species present within the limits of the UK and Irish continental shelf region and show which deep-sea coral habitats are currently protected in the North-east Atlantic between 46-63°N, and which are not.

Nile damming as plausible cause of long-term changes in deep-sea Mediterranean communities over broad spatial scales

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ICM CSIC

Nile River damming in 1964 (after the Aswan Dam construction) induced important oceanographic changes in intermediate and deep waters (>150 m) of the Mediterranean Sea also inducing a wide range of ecological impacts. The giant shrimp *Aristaeomorpha foliacea* has become locally extinct off Catalonian coasts (and in the northwestern Mediterranean) at 400-900 m, with a simultaneous drop in the catches of red shrimp, *Aristeus antennatus*, in the second half of the 1960s (based on data series starting in the 1940s/50s). The sharp decline of deep-shrimp off Catalonian coast (3200 km westwards from Nile Delta) followed the 1964 drop in Nile discharge with a delay of 3 to 5 years. The Levantine Intermediate Water (LIW),

which broadly overlaps with the depth range inhabited by *A. foliacea*, had significant salinity (S) increases in the 1950s-1970s, and Nile damming has contributed about 45% of the total S increase of deep-water masses from the 1960s to now. Other factors further reduced freshwater flow into the Mediterranean Sea hence increasing LIW salinity, and Nile damming was probably a triggering factor for the extinction/drop of deep-sea shrimp. These same impacts, together with the increase of fishing effort, may also induce changes in the whole deep-water assemblages at LIW domains. We found significant changes in slope assemblages before (1950s-1960s) and after (1970s to 2007) the date of Nile damming, after analyzing information from ca. 60 commercial hauls in/close to the Balearic Basin at depths between 300 and 600 m. In spite that some local factors (e.g. canyon influence) have also some effects on our analyses, the decline of *A. foliacea* in the last 60s in the north-western Mediterranean could also be extensible to the rarefaction of some bathyal sharks, especially *Etmopterus spinax*, an ovoviviparous shark probably highly vulnerable to changes in ecosystems.

Genetic diversity and length distribution of the offshore rockfish (*Pontinus kuhlii*) from three Atlantic archipelagos

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The offshore rockfish (*Pontinus kuhlii*) is a widespread demersal fish in the temperate eastern Atlantic. This species inhabits hard bottoms at depths between 100 and 600 meters and is an important resource for the Azorean commercial fleet. During several fishing campaigns, which took place in the Azores, Madeira and Cape Verde archipelagos, including several seamounts, diverse biological data on this species was collected. In this work we compare the length distributions, total catches and vertical distributions in order to evaluate the abundance, population structure and possible differences in habitats choices in the three archipelagos. Furthermore, once this species appear to have a sedentary behaviour and its vertical distribution is relatively limited it is expected that depth could act as a barrier for the connectivity and gene flow between populations of this species. The use different molecular markers, mitochondrial D-loop and cytb and nuclear S7, will shade some light on population structure for the *P. kuhlii*.

Organic osmolytes in deep-sea coral

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Most marine organisms osmoconform with seawater in part by using organic osmolytes in their cells; in addition to providing osmotic pressure, some osmolytes counteract the effects of environmental stresses. We have found that deep-sea crustaceans, anemones and

elasmobranch fish have different osmolytes than do their shallow relatives, possibly to protect proteins from the destabilizing effects of hydrostatic pressure. Recently we characterized the osmolytes of shallow symbiont-bearing tropical corals (7 species), and found they were primarily methylated solutes: glycine betaine, proline betaine and dimethylsulfoniopropionate (DMSP), with glycine betaine consisting of more than 90% of the osmotic pool in most species. Here we report new analyses of deep-sea, non-symbiotic corals (*Flabellum impensum*, *Enallopsammia rostrata*, *Desmophyllum dianthus*, *Caryophyllia* sp.), from 9 different sites on New England and Antarctic seamounts at 600 to 2600 m depths. Using high performance liquid chromatography, we found the major osmolyte to be glycine betaine in all species, with the solute composition of the 600 m corals being very similar to that of shallow corals. However, there were also several organic solutes contributing significantly to osmotic pressure that increased with depth. Some of these solutes are yet to be identified, but are the same as those we have found in deep (but not shallow) mollusks. In the deepest species (*Caryophyllia*), one of these solutes was scyllo-inositol, an unusual sugar with protein-stabilizing properties that we have previously found in deep-sea (but not shallow) anemones and echinoderms. Thus there may be organic osmolytes in deep-sea corals involved in adaptation to the deep sea.

A global seamount classification to aid the scientific design of marine protected area networks

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Seamounts are prominent features of the world's seafloor, and are the target of deep-sea commercial fisheries, and of interest for minerals exploitation. They can host vulnerable benthic communities, which can be rapidly and severely impacted by human activities. There have been recent calls to establish networks of marine protected areas on the High Seas, including seamounts. However, there is little biological information on the benthic communities on seamounts, and this has limited the ability of scientists to inform managers about seamounts that should be protected as part of a network. In this paper we present examples of seamount classification systems based on "biologically meaningful" physical variables for which global-scale or regional data are available. The approach involves the use of key environmental variables (e.g., overlying export production, summit depth, oxygen levels, seamount proximity) to group seamounts with similar characteristics. This procedure can be done in a simple hierarchical manner, or using multivariate methods. The approach can give biologically realistic groupings, in a transparent process that can be used to either directly select, or aid selection of, seamounts to be protected.

Trophodynamic studies of the CONDOR seamount (Azores, Portugal, North Atlantic)

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Seamounts are widespread and abundant topographic features of the world's oceans and yet knowledge on their biodiversity and ecosystem functioning are scarce. They are common features in the Azores archipelago EEZ and are extremely important ecosystems in the region, as hotspots of marine life and for fisheries. CONDOR is a multidisciplinary project which integrates scientific research, management and public outreach. This integrated project is implementing an underwater observatory on the Condor seamount, in the Azores, for a better understanding of oceanographic and biological processes occurring at seamounts.

Seamount ecosystem trophic structure and functioning was studied covering the pelagic environment (zooplankton, ichthyoplankton, mesopelagic organisms and top predators and the sea bed habitats (demersal fishes and benthonic macrofauna). Stable carbon and nitrogen isotopic signatures were determined on these species and compared to other samples from the Mid-Atlantic Ridge (South and North of the Azores). The values overlap and cover a large range within feeding types, indicating a strong overlap in food sources and a high degree of competition for food. The highly mobile benthopelagic predators/scavengers, are at the top trophic position with the higher nitrogen values, and represent a major link with the benthopelagic food web through their feeding on pelagic prey. Trophic guilds were established, and the role of fishes on the benthic hardrock fauna was investigated.

Metabolism and trophic levels of benthic and benthopelagic chondrichthyan fishes off the coast of California

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Ecologically, there is a great need to understand the energy requirements of understudied marine taxa, such as bottom-dwelling chondrichthyans. Information on species metabolism, burst locomotory capability, and energy requirements are key factors in the understanding of ecosystem dynamics with depth. Chondrichthyans are faced with increasing fishing pressure in the deep-sea with effects that appear to have already reached the maximum attainable depths known for these species. Thus, the potential depletion of these upper trophic level fishes may occur before they are understood, and may have unknown long-term ecological implications. Currently, very little is known about the metabolic rates of deep-sea chondrichthyans. We will present data for 12 species of sharks, skates and chimaeras collected off the coast of Monterey, California at depths of 100 to 2000 m. Biochemical indices of aerobic (citrate synthase and malate dehydrogenase) and anaerobic (lactate dehydrogenase and pyruvate kinase) metabolism are analyzed in red and white muscle tissues in order to elucidate whole animal metabolism and burst locomotory capability. Studying the roles of these top-predators is essential to the understanding of large-scale population dynamics, energy transfer with depth, and potential implementation of ecosystem-based, deep-sea fisheries management.

The International Seabed Authority and marine scientific research

Cook A.A.

International Seabed Authority

The International Seabed Authority is an autonomous international organization established as part of the United Nations Convention on the Law of the Sea. The Authority is the organization through which governments organize and control activities in the seabed beyond limits of national jurisdiction, particularly with a view to administering the mineral resources of the Area. The resources that the Authority is concerned with are polymetallic nodules (found on abyssal plains), cobalt-rich crusts (found on seamounts) and polymetallic sulphides (found near hydrothermal vents). Any mineral resource found in the future will also come under the remit of the Authority.

In addition to administering the resources of the seabed, the Authority must ensure that the environment is not unduly harmed during mining activities. To do this the Authority seeks the advice of scientists when preparing environmental guidelines for contractors and when carrying out periodic review of these guidelines. In addition, the International Seabed Authority has a role to promote and encourage marine scientific research in areas beyond national jurisdiction and the dissemination of the results of such endeavours.

One of the ways in which the Authority has fulfilled its mandate in the promotion and encouragement of marine scientific research has been by establishing The International Seabed Authority Endowment Fund. The aim of the Fund is to encourage the conduct of collaborative marine scientific research in the international seabed area by supporting the participation of qualified scientists and technical personnel from developing countries in marine scientific research programmes and activities. Any appropriate scientists or research groups are encouraged to submit applications for funding. Full details can be found on the Fund's website (<http://www.isa.org.jm/en/efund/fund>).

The Authority also seeks to develop existing relationships and establish new collaborations with scientists and their institutions in order to gain a better understanding of the environments where commercially exploitable minerals are found beyond national jurisdiction.

Examination of bathymetric patterns of deep-sea communities in a hydrocarbon-seep ecosystem

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There are well established bathymetric patterns in biomass, density and diversity of deep-sea soft-bottom communities. In general, biomass and density decline with depth, and diversity is highest on the mid-slope. Patterns in biomass and density of deep-sea communities have primarily been attributed to food availability. The modal distribution of diversity is potentially related to trophic factors, but it has also been attributed to pressure and temperature effects on species distributions. In this study, these bathymetric patterns are examined in cold seep communities from 500 to 3300 m depth in the Gulf of Mexico. By analyzing data from cold seep communities that are primarily fueled by local chemosynthetic productivity, the influence of food availability is largely removed. On 10 cruises between 1995 and 2007, a total of 97 different mussel-bed and tubeworm-aggregation associated communities were sampled at 25 cold seep sites with the HOV Johnson Sea-Link, HOV Alvin, and ROV Jason II. Although species composition changes dramatically over this depth range, there is no apparent decline in density or biomass with depth in the communities. There is some evidence for a mid-slope diversity maximum in alpha diversity and an elevation in beta diversity at the deeper sites of the lower slope. However, the bathymetric patterns in diversity differ between mussel and tubeworm associated communities. The slight elevation in alpha diversity estimates for the mid-slope communities may result from the overlapping bathymetric distribution of many of the upper and lower slope seep species. These results support the hypothesis that bathymetric declines in density and biomass of the general deep-sea fauna are related to the decline in food availability, although trends in diversity appear to be driven by other factors.

Diversity of macrofauna assemblages from three Portuguese submarine canyons (NE Atlantic)

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The macrofauna assemblages from three Portuguese submarine canyons, Nazaré, Cascais and Setúbal were studied from samples collected at their upper (900-1000 m), middle (3200-3500 m) and lower sections (4200-4500 m) and at the adjacent open slopes (~1000 m), during the

HERMES cruises D297 (RRS Discovery, 2005) CD179 (RRS Charles Darwin, 2006) and 64PE252 (RV Pelagia, 2006). The benthic macrofauna of the Portuguese canyons showed important variations in taxonomic and functional composition, abundance, diversity and community structure. Multivariate analyses showed significant differences between and within canyons and between canyons and open slope assemblages. Abundance in the upper canyons was significantly higher than in the adjacent slopes and in all canyons the bathymetric trend was identical with peak abundances occurring at intermediate depths. Lower diversity, coupled with high dominance, occurred in the middle section of the Nazaré and Setúbal canyons, but high diversity and low dominance were maintained along the depth gradient in the Cascais Canyon. Overall, the Nazaré Canyon showed the lowest Hurlbert's expected species richness (E(S100): 16-39) and Cascais Canyon the highest (39-54). There was a positive correlation between macrofauna abundance and sediment total nitrogen concentration, and a negative correlation between diversity and sediment total organic carbon. This indicates that organic loading is probably the major driver for structuring canyon benthic assemblages. Diversity is likely to be maintained by variations in food availability and partitioning of resources by different species. Altered and localised environmental conditions in the Portuguese canyons play an important role and overwrite more general abundance and diversity bathymetric patterns. The present study suggests that canyons may show multiple patterns of biodiversity in relation to the adjacent margins, generated by complex interactions of several environmental drivers and the differential response of organisms and populations.

Enhanced macrofaunal abundance and beta diversity in three Hawaiian submarine canyons: deep-sea oases embedded in an oligotrophic ocean

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To explore the role of submarine canyons as biomass hotspots in oligotrophic oceans, we sampled macrofaunal communities in three submarine canyons and on nearby slopes on the islands of Oahu and Moloka'i. We hypothesized that canyons on oceanic islands in the oligotrophic North Pacific gyre enhance macrofaunal abundance and regional biodiversity by concentrating coastally-derived detrital organic matter and increasing habitat heterogeneity. A total of 121 sediment cores (7.6 cm diameter) were collected by submersibles in a sampling design stratified by depth (350, 650, 1000, and 1500 m), habitat (canyons vs. open slope) and island. Samples were sorted to species and community abundance, alpha (local) diversity, and beta diversity (species turnover) was compared across habitats and depths. We found significantly higher macrofaunal abundance in canyons at all depths with the most profound differences at 650 and 1000 m. Both alpha diversity (sample species richness and Shannon diversity) and beta diversity were much higher in canyons, particularly at the deeper stations. Ordination (n-MDS) and similarity (ANOSIM) analyses revealed marked differences in community composition between canyons and slopes as well as between the islands of Moloka'i and Oahu. Opportunistic polychaete families (e.g., Capitellidae and Spionidae) dominated the fauna in canyon sites while bivalves, aplacophorans and omnivorous polychaete families dominated slopes. Our results are consistent with the hypothesis that

submarine canyons enhance biodiversity due to higher food availability and increased habitat heterogeneity. These results indicate that canyons on oceanic islands can be important hotspots of biodiversity and merit targeting in marine conservation strategies.

Quantitative assessment of deep-sea fish communities off Hawaii: the effect of submarine canyons and habitat structure on assemblage abundance and composition

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Canyons can be sites of enhanced fish biomass and productivity on continental and island margins. We used high-definition video surveys to investigate demersal fish assemblages in two submarine canyons off the island of Moloka'i, Hawaii. We investigated the correlations between habitat type (e.g., highly structured within canyons and highly homogeneous on slopes) and the abundance and composition of the fish assemblage. The surveys were performed during 11 dives using the NOAA-HURL Pisces V submersible at depths from 350 to 1050 m in canyon and slope habitats. A total of 47 transects (3-5 replicates per site) were completed with constant submersible speeds of 2 knots and transect durations of 9-24 min to determine species composition and abundance. Fish were identified to the lowest possible taxonomic level and assigned to operational taxonomic units (OTUs). For each fish observed, bottom habitat type was also categorized (e.g., mud, sand, sand with ripples, sand with boulders, rock outcrops; gentle, mid or steep slope) and assigned to each fish observation to elucidate habitat preferences. A total of 930 fishes were observed during ~13 hours of video yielding a total of 86 OTUs. Macrouridae was the most diverse family. Community composition was substantially different between depths within canyon sites with chlorophthalmids dominating at 350 m, macrourids and synphobranchids at intermediate depths (650 m), and halosaurs at 1050 m. Communities also differed between canyon and slope habitats, with indications of bottom habitat preferences. Abundances were generally higher in the canyon sites, however only statistically significantly so at the deepest sites. The fish densities observed in canyons of 0.5-1.5 fish per 100 m² are comparable to densities observed on continental margins off California, a much more eutrophic marine ecosystem. These results suggest that canyons channel detrital organic matter sources to fuel deep-sea food webs on Hawaiian island margins.

Trace metal bioaccumulation in mussel's and clam's shells at the deep-sea hydrothermal vent fields

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The *Bathymodiolus* spp. mussels and *Calyptogena magnifica* clams are known to be a dominant organisms which inhabit the deep-sea hydrothermal vent fields. The peculiarities of the trace metals accumulation in carbonate shells of mussels and clams were studied in 46 samples collected at six geochemically different hydrothermal vent fields of the Middle-Atlantic Ridge (Menez Gwen, Rainbow, Broken Spur, Snake-Pit), as well as of the East-Pacific Rise (9°50' N, Guaymas Basin). Determination of distribution patterns of Fe, Mn, Zn, Cu, Cd, Pb, Ag, Ni, Cr, Co, As, Se, Sb and Hg in shells along with in water of biotope gave an evidence of environmental and biological parameters' influence on their bioaccumulation. Mussels and clams from the high temperature hydrothermal vent fields concentrate in their shells Fe and Mn as much as 20-30 times more than mussels from the low temperature Menez Gwen vent field where the near bottom water is depleted in trace metals compared to the high temperature vent fields. More intensive accumulation of essential trace metals (Fe, Mn, Ni and Cu) was revealed for the early ontogeny stage of the *Bathymodiolus azoricus* mussels. The passive trace metal accumulation due to the adsorption processes on the shells' surfaces reaches up to 50% from the total content in shells, varying from 14 % (Fe) to 46% (Mn). From high concentration coefficients ($n \cdot 10^2$ - $n \cdot 10^4$) of majority of trace metals in carbonate shells and the fact that they have a biomass several times more than that of the soft tissues, we may to conclude about powerful accumulation function of the hydrothermal bivalve mollusks shells.

Zooplankton at a seamount in the Eastern Mediterranean: distribution and trophic interactions

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The study addresses the possible effects of steep topography on the zooplankton community in the oligotrophic eastern Mediterranean. Zooplankton, along with hydrographical data, was sampled with 333 μm nets at two sites, the Anaximenes Mountain, a seamount-like structure in the northern Levantine Basin, and the deep Rhodes Basin as reference location. The samples were sieved into size fractions, and the composition, biomass, abundance and stable isotope signatures were analyzed. In general, biomass and abundance of zooplankton were low, reflecting the oligotrophic character of the eastern Mediterranean, but zooplankton standing stocks were higher in the Rhodes Basin than at the Anaximenes Mountain. The taxonomic composition above the seamount summit did not differ markedly from the slope region or the reference station, and no difference in size structure could be observed. Stable isotope signatures showed, at a generally low level, enrichment in zooplankton taxa along the

food chain within the different pelagic zones and from the surface to the deep-sea, but no significant differences between Rhodes Basin and the seamount were evident in the food web structure. The zooplankton community in the Anaximenes Mountain region seems not to be influenced by a local seamount effect, but differences in standing stocks between the seamount and the Rhodes Basin are more likely driven by larger-scale upwelling and downwelling structures of cyclonic and anticyclonic eddies and gyres, which dominate the circulation in the area. The results will be compared to first data from a recent cruise to Eratosthenes Seamount, a large seamount south of Cyprus.

Composition and distribution of the deep-sea benthic fauna off Western Galicia (NW Iberian Peninsula)

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The rias and shallow coastal areas of Galicia (NW Iberian Peninsula) are characterized by a great variety of benthic habitats which results in diverse faunal assemblages. Furthermore, these areas have a great economic significance due to the existence of fisheries and mussel culture on rafts. However, the deep bottoms of this region are still very little known both ecologically and taxonomically. In June and September 2008 two oceanographic expeditions (A SELVA and DIVA-ARTABRIA II) were carried out on the coasts of Galicia to study the deep-sea benthic biodiversity of this region. Samples were collected by using different types of dredges (Agassiz trawl, a modified Epibenthic sledge and a Naturalist's dredge) depending on the type of substratum. The samples were sieved and sorted out on board and then fixed with buffered formalin and preserved in 70% alcohol. The largest specimens of 2 mm were classified into the different zoological groups and quantified for each station. In this poster, the first results of diversity and distribution of macrofaunal assemblages of two large areas sampled during these expeditions (A Quiniela and A Selva), which comprise some areas both of the continental shelf and slope, are presented.

Scavenging amphipods in deep-sea canyon ecosystems

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The high degree of heterogeneity found both between and within submarine canyons makes them of particular interest to researchers studying the deep sea. Their role as sediment traps, intercepting suspended material being laterally transported across the continental shelf, makes them hotspots of secondary production with distinct faunal assemblages and idiosyncratic ecosystems. Sampling deep-sea canyons using trawls is both difficult and destructive, however via the exploitation of their natural foraging behaviour it is relatively easy and cost-effective to collect large samples of scavenging amphipods from canyon sites using baited traps. Fourteen freefall baited traps were set at different depths within three submarine canyons on the Portuguese Margin (Nazaré, Setúbal, and Cascais). The collected amphipods were preserved and stored for identification to species level and measurement of a number of indices to enable comparison of populations. Statistical analysis of these data will allow for comparison of scavenging amphipod assemblages at different depths within each canyon and between different canyon ecosystems. It is anticipated that during the PhD, further baited-trap samples will be obtained from new submarine canyon systems and also that further data will be collected from the Portuguese Margin canyons to enable a study of change with time and season. This research will further the understanding of differences in biodiversity between deep-sea canyons while also potentially identifying endemic canyon species.

Quantifying the diet composition and guild structure of deep-sea fishes

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There is a growing awareness that quantifying the interactions between fish species can help management for sustainable fisheries. On Chatham Rise, to the east of New Zealand, nearly 12,000 stomachs were sampled over 3 years from 31 fish and squid species, at depths of 200-1000 m. The diets of most of the species had not been studied in detail before. Stomachs were examined for prey in the laboratory, and about 100,000 individual prey of 340 prey groups recorded. A set of biological and environmental statistics were tested as potential predictors of diet variability using distance based linear models. Each species diet varied significantly with one or more predictors from; fish size, sex, location (longitude, latitude, depth), time (year, time of day, moon phase), and sampling source (research or commercial vessel). Different mechanisms for avoiding resource competition between related species were identified, and included dietary specialisation in macrourids, and spatial separation in chimaeras. Discarded offal from fishing vessels was an important food source for several species. Potential intraguild predation was identified between some important commercial species. Cluster analysis identified ten trophic guilds falling into four broad groups: benthopelagic and mesopelagic foragers; piscivores; salp specialists; and predominantly benthic foragers. A key challenge for scientists is to determine how diet and guild information can now be used to assist fisheries management.

Ciliate-bacterial symbiosis: A cooperative strategy in low oxygen, sulfidic marine sediments?

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WHOI

Marine micro-oxic to sulfidic environments are sites of intensive biogeochemical cycling and elemental sequestration, where prokaryotes are major driving forces mediating carbon, nitrogen, sulfur, phosphorus, and metal cycles, important from both biogeochemical and evolutionary perspectives. Associations between single-celled eukaryotes and prokaryotes are common here, especially among ciliates and flagellates. Previously described partners include purple non-sulfur photosynthetic bacteria, methanogenic archaea, as well as putative ectosymbiotic sulfate-reducing and sulfide-oxidizing bacteria. Here we describe a ciliate common to the micro-oxic, anoxic, and sulfidic sediments of Santa Barbara Basin. The ciliate, which is brown, is 94% similar to *Parduzcia orbis* (18S rRNA). Transmission electron micrographs reveal clusters of at least three different endobiont morphotypes organized within membrane-bound sub-cellular regions. CARD-FISH and 16S rRNA clone libraries confirm the symbionts include at least one sulfate reducer (Desulfobacteracea and Desulfobulbaceae), a probable Bacteroidete (Cytophaga), and a methanogen (Methanobacteriales) suggesting a complex cooperative strategy for energy metabolism in this environment.

Deep-sea isopod biodiversity and distribution in the Sea of Japan and the Kuril–Kamchatka area

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The Sea of Japan in the Northwest Pacific has some unique characteristics: it is shallower than the adjacent marginal seas like the Sea of Okhotsk and the East China Sea. In contrast to these which are connected to the Pacific through deep-water straits, it is separated from the Pacific Ocean with the exception of shallow water straits which do not exceed 130 m water depth. During the Pleistocene, the Sea of Japan became anoxic due to sea level decline below this depth during glacial maximum. The biological succession regarding the abyssal plains after this phase is unknown as well as the abyssal fauna in this area. Only one species, *Mirabilicoxa kussakini* (Isopoda: Desmosomatidae), is recorded from the abyssal plains of the Sea of Japan. In order to investigate this biologically unknown area, a Russian-German cruise with the RV Akademik Lavrentyev will take samples with a modified epibenthic sledge. To compare the fauna of the isolated area of the Sea of Japan with the one of the open Pacific, in 2012 a German-Russian cruise with the RV Sonne will take samples with the same gear to the abyssal plain of the Kuril-Kamchatka Trench, where also some stations sampled by Russian

scientists in 1954 and 1966 will be re-sampled. Until now 70 isopod species are known from that area and we hypothesise: 1. that we will find a much higher number of species due to improved sampling methods; 2. that isopod species richness is much higher in the non-isolated deep sea of the Kurile Kamchatka area compared to the relatively isolated deep sea of the Sea of Japan. These expeditions are contributing to the CoML project CeDAMar (Census of the Diversity of Abyssal Marine Life) which will be continued beyond the first Census of the Marine Life which will end in October of 2010.

Long term, deep water sediment trap moorings at contrasting productivity environments in the Southern Ocean, Antarctica

Enderlein Peter and Pond David

British Antarctic Survey

Two deep water moorings with a scientific payload of sediment traps, current meters, CTDs and ADCPs have been deployed in deep water locations (3200 m and 3700 m) in the Southern Ocean since November 2006. The aim of this poster is to present the first results from the sediment trap collections on the biogeochemical export processes of the epipelagic zone over multiyear time scales. One sediment trap mooring was located in a low productivity system immediately upstream of South Georgia, whilst a second was located downstream of South Georgia in iron enriched, high productivity waters. Material collected by the sediment traps at both sites was dominated by diatoms, pteropods and foraminifera, the abundance of which varied seasonally. Zooplankton faecal pellets were also present but never abundant. Overall, export of key biogeochemical elements was linked to both primary productivity and food web structure in the two productivity systems.

Understanding population connectivity in the deep sea: phylogeographic patterns in Ophiuroids from around Australia and New Zealand

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Our knowledge about connectivity between populations of bathyal invertebrates is limited in taxonomic scope and regional coverage. The results of phylogeographic investigations into five ophiuroids, collected from a 8000 km wide sector across southern Australia and New Zealand, showed that mitochondrial genetic diversity was often remarkably low, with common haplotypes spread across the study region. This included species with lecithotrophic larvae and even a seamount specialist that broods! Cryptic speciation was evident in several taxa, with cryptic species variously separated by latitude, longitude or depth. Estimates of population connectivity are compared with estimates of physical connectivity derived from general circulation models.

Benthic macrofauna on methane-related features in the Gulf of Cádiz: preliminary results from MVSEIS08 cruise

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Many seafloor features associated with methane seepage have been identified and studied on the Gulf of Cádiz in the recent years, including pockmarks, mud volcanoes and methane-derived authigenic carbonates. During the MVSEIS08 cruise (May 2008), high resolution seismic profiles, multi-beam bathymetric images, gravity corers and dredging samples were obtained for a comprehensive and multidisciplinary research of these features. Epifaunal specimens were collected from the dredges, and also the gravity corers permitted to record some infaunal, chemosynthetic species. According to the geologic and oceanographic characteristics of the seabed and the presence or abundance of certain species, we could establish the following classification of the samples:

- Samples with abundant, large authigenic carbonates (e.g. crusts, slabs or chimneys), on sites affected by the Mediterranean Outflow Water contour current: Those sites were characterized for presenting large colonies of the anthipatarian *Leiopathes glaberrima*, numerous although small sized colonies of the alcyonacean families Plexauridae and Paragorgiidae and several specimens of the echinid *Cidaris* spp. and the bivalve *Limopsis aurita*.
- Samples that included fragments of carbonate crusts, nodules, and mud breccia or anoxic or green mud, and situated on the Moroccan slope: Isididae alcyonaceans appeared on those samples. Serpulidae Polychaetes and bryozoans were the most frequent groups over the crusts and nodules, and high numbers of *Siboglinum* spp. were found in the mud. Other groups present were Onuphidae and Hesionidae polychaetes, decapod crustaceans, ophiurids and crinoids.
- Samples taken on mud volcanoes or nearby, which included a significative proportion of mud breccia, and often accompanied by rests of corals and empty shells: The very high densities of *Siboglinum* spp. were the most remarkable characteristic. The deep faunal communities in the Gulf of Cádiz are thus strongly determined by the geological characteristics of the seafloor, but heavily influenced by the physical environment.

The occurrence of some mesopelagic, bathypelagic, and cold-water cosmopolitan species of holoplanktonic polychaetes in the Eastern Tropical Pacific Ocean

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The zoogeography knowledge of pelagic regions in the open ocean is generally scarce, particularly that from deeper waters. Ekman (1953) suggested that this marine fauna followed world-wide distribution patterns and recognized some biogeographic regions, considering that

temperature is one of the most important parameter determining their extent. An important fact of these patterns is the vast distribution of the pelagic animals, some of them considered as cosmopolitan species. Ekman discussed the meaning of this term and distinguished two main groups, one eurythermal and other more or less stenothermal. The species of the last group have a widespread distribution, but avoid the warm surface water in tropical regions by submergence, living thus in deeper waters in this area. He mentioned that the holoplanktonic polychaete *Tomopteris septentrionalis* (Tomopteridae) is a good example of these group of animals. This species was recorded in some few localities in the Eastern Tropical Pacific Ocean, where the isotherm of 15°C was above the 200 m deep. The same situation was found for the polychaete *Vanadis tagensis* (Alciopidae) and *Tomopteris krampi* which have been considered as mesopelagic and bathypelagic species, respectively. The presence of these three species in a tropical region is discussed from a biogeographical point of view taking into account results of 579 zooplankton samples which were collected over an extensive area (20°N to 20°S, and the coast of America continent westward to longitud 126°W). This is an important region of the Pacific that supports valuable fisheries. Sampling was performed through the EASTROPAC Oceanographic Program during 12 cruises carried out in five periods between January–September 1967 and January–April 1968.

Deep-water octocorals of the Bahamas bathyal slope (Western North Atlantic) and their relationship to offshore seamount assemblages

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In March 2009 we led an expedition to sample and record (video and still imagery) deep-sea coral communities on the Bahamas bathyal slope using the Global Explorer ROV operated from the R/V F.G. Walton Smith. We conducted 14 ROV dives between 800-2327 meters depth at 12 locations – 6 on the Atlantic basin slope and 6 in the channels and basins of the Bahama Platform –recording 110 hours of DVCam video, >7 hours of high definition video, and ≈100GB of digital images (HD video frame grabs and digital still photographs). Collections of 97 octocorals and their associate fauna (notably ophiuroids, polychaetes, galatheids and shrimp) were made for taxonomic identification, vouchering and genetic analyses. The diversity of octocorals in this region was higher than expected, and was dominated by species from two families: Isididae (bamboo corals) and Chrysogorgiidae. Despite the relatively small area surveyed, genetic data suggest we found at least 13 isidid and 10 chrysogorgiid species. Of the isidids, 6 were previously collected in the western North Atlantic (4 on the New England Seamounts, 1 from the Corner Seamounts, 1 from Gilbert Canyon). Eleven bamboo coral haplotypes (putative species) collected on the New England Seamounts were not seen among Bahamas collections. There are only a dozen nominal bamboo coral species known from the entire North Atlantic and thus this diversity likely includes species new to science. Among the 10 chrysogorgiid species, 6 were sampled previously on the NES, including *Metallogorgia melanotrichos*, which had not previously been recorded from the continental margin, but in this area was relatively common. Because much of this area is characterized by very steep, rugged topography, octocorals are unlikely to

be collected – at least whole – by scientific dredging or trawling, particularly the isidids, many of which had thin skeletons resulting in fragile colonies.

Metabolism and gill morphology of benthic fish species associated with the oxygen minimum zone within Monterey Bay, California

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Oxygen minimum zones (OMZs) are temporally and spatially persistent mid-water regions of reduced dissolved oxygen content. The reduced oxygen concentration presents a distributional boundary for many benthic species where OMZs impinge upon the continental margin, resulting in reduced megafaunal diversity and biomass in the core of the minima zone. Recent observations have shown vertical expansions of these minima zones over the past few decades, making our knowledge of adaptive morphology and physiology of OMZ-associated fauna extremely pertinent. Previous studies have investigated the adaptations of benthic invertebrates and pelagic fishes to the reduced oxygen concentration. This study will evaluate metabolic and respiratory adaptations of demersal fishes collected off central California (Monterey Bay) to the OMZ. Fishes are grouped into four categories based on depth distribution (species living shallower than, species living within, and species living deeper than the minima, in addition to species whose depth distributions range throughout all depth categories) with representatives from five families (Scorpaenidae, Macrouridae, Lipariidae, Pleuronectidae and Anoplopomatidae). We will present anaerobic (lactate dehydrogenase, pyruvate kinase) and aerobic (malate dehydrogenase, citrate synthase) enzymatic activity data for red, white and cardiac muscle tissue in order to assess whole animal metabolic poise and oxygen tolerance. Also, gill morphometric measurements will be presented in order to estimate gill surface area, as a proxy for the ability to extract oxygen.

The Occurrence of Liparids (snailfish) at Depths below 6000 m in Multiple Trench Ecosystems and the Abundance and Diversity of Hadal Fishes

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Using an ultra-deep free falling camera system, the HADEEP project has been undertaking direct study on the distribution and behaviour of the deepest-living scavenging fauna at hadal depths situated primarily within oceanic trenches which plummet from 6000 m to the full ocean depth of almost 11,000 m. These are the deepest habitats on earth which may represent only a small fraction of space in area (< 1%), yet account for as much as 45% of the oceanic vertical depth gradient. Since 2007, we have conducted standardised baited camera deployments across five trenches in the West Pacific Rim to further understanding of the bathymetric and biogeographical distribution of hadal fauna at intra- and inter-trench levels. Here we present the deepest known in situ observations of hadal snailfish, *Pseudoliparis*

amblystomopsis (liparidae), from 7703 m in the Japan Trench (NW Pacific), and these will be compared with our most recent finding of *Notoliparis kermadecensis* (liparidae) from 7561 m in the Kermadec Trench (SW Pacific). The maximum numbers of these snailfishes observed were unexpectedly higher than historical trawl catch records of any known hadal fish, and they were observed to efficiently prey upon fast swimming mobile amphipods. In light of these new observations we have reappraised the occurrence and diversity of hadal fishes that have been constructed on fragmentary and often misleading information derived from historical explorations and global data sets. The reanalysis suggests that the current record of hadal fish diversity is likely to be an overestimate, but some hadal fish species are capable of attaining much larger populations in places than previously anticipated. Liparids are likely to play an important role in structuring hadal food web in trench ecosystems and this presentation will point towards newly emerging directions for future research in both deep-sea fish and hadal trench ecology.

Megabenthic community of the Håkon Mosby mud volcano: preliminary results of image analysis

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The Håkon Mosby mud volcano (Barents Sea, depth ca. 1270 m) was studied in August 2002 by the RV Polarstern expedition ARKXVIII/1b using the Ocean Floor Observation System (OFOS). Different habitats of the volcano and the background were inspected and photographed at three OFOS transects. The aim of our study was to evaluate the influence of mud volcano on the abundance and distribution of megabenthic fauna. Based on examination of 1369 images, 42 objects including animals, bacterial mats and seafloor characters were identified and quantified per meter square. The analysis revealed significant differences between benthic communities from different habitats. The background community was numerically dominated by ophiuroids *Ohiocten gracilis* associated with oxidized light-colour sediment and only occasionally penetrating the central part of volcano. Most of observed taxa (echinoids, starfishes, crinoids a.o.) avoided areas of active methane discharge, whereas some were most abundant in the zone of moderate seepage marked by colonies of pogonophorans *Archeolinum contortum* and *Oligobrachia webbi*. The relative abundance of pycnogonids *Nymphon macronix*, caprellids *Metacaprella horrida*, unidentified small amphipods and thyasirid bivalves distinctly increased on pogonophoran fields. In areas covered by extensive bacterial mats (>50% cover), the abundance of benthic species generally decreased. The fish *Licodes squamiventer* was the most abundant in areas of patchy or continuous bacterial mats. Part of the flat caldera centre known as a region of intensive methane discharge was nearly devoid of benthic communities. Some of observed species (mostly relatively large mobile crustaceans and fishes) were present throughout the observed area do not forming clear associations with any specific habitat.

Data about two new species of Mollusca Solenogastres from Antarctic Peninsula and Bellingshausen Sea (Bentart-2006 Expedition)

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The research programme for the study of the Antarctic benthos Bentart-2006 was carried out during January and March 2006 in the waters of the Bellingshausen Sea and the Antarctic Peninsula on board the R/V Hespérides. Solenogastres are vermiform Mollusca with a mantle covered with sclerites and a foot converted into a ventral groove. Nearly 50% of the 260 known species are Antarctic and information on their biology, diversity and geographical distribution are extremely limited and inconsistent. In this communication we present the first data about two new species of *Neomenia* Tullberg, 1875 and *Amboherpia* Handl & Salvini-Plawen, 2002 collected at a depth of 400-1300 m. *Neomenia* sp. Antarctic Peninsula (65°16.654'S; 68°9.364'W). Water depth: 1272 m. Body up to 3.4 cm x 0.95 cm. With 5-7 longitudinal keels. Thick cuticle (270 µm). Three types sclerites with radial insertion: groove-shaped sclerites without spear-shaped distal end, solid, slightly bent needles, and solid blade-shaped scales. Pedal groove with 25-35 ciliated folds. Pharynx with three regions. With vesicle and receptacle seminal. Paired secondary genital opening. With spawning duct gland and stylet gland. Two paired copulatory stylets. With suprapallial glands. Without pre-pallial spines. 40-45 gill folds. A dorso-terminal sense organ. *Amboherpia* sp. Bellingshausen Sea. (70°28.911'S; 84°2.841'W). Water depth: 430 m. Body up to 3 mm x 0.40 mm. Without longitudinal keels. Thin cuticle (15-20 µm). Two types sclerites: hollow acicular sclerites and groove-shaped scales. Pedal groove with a ciliated fold. Monoserial radula. With oesophagus. Ventral foregut glandular organs type *Acanthomenia*. Unpaired secondary genital opening. Without respiratory folds. Without copulatory stylets. With a dorso-terminal sense organ.

Distribution of cumaceans (Crustacea, Peracarida) in the continental shelf and slope of Golfo Ártabro (Galicia, NW Iberian Peninsula)

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The composition and distribution of benthic assemblages in the intertidal zone and shallow waters of the continental shelf of Galician coast is well-documented but fauna from deeper areas have been less studied. Cumaceans (Crustacea, Peracarida) show a greater diversity at the deep sea than at shallow waters. In Galician waters, cumaceans are, in general, among the less known peracarid taxa, mainly because of a lack of specialists and projects devoted to the study of this zoological group. In 2002, the Marine Biological Station of A Graña (Universidade de Santiago de Compostela, Spain) started the 'DIVA-Artabria I' project as a survey of the benthic fauna of the Galician shelf and slope off Golfo Ártabro (NW Spain) in order to obtain baseline data about diversity, composition and distribution of benthic assemblages. In September 2002, the first 'DIVA-Artabria I' expedition was done. One

additional expedition was later done in the same area in 2003. Sampling stations were located along a transect starting at depths of 150 m in the continental shelf and crossing the continental slope in NW direction to depths of about 1,000 m. Three different sampling gears were deployed depending on the nature of the substratum: Agassiz Trawl, Naturalist dredge and Epibenthic sledge. Sandy-muddy sediments are present at the continental shelf while the slope is characterized by hard substrata such as stones, corals and carbonated formations. In this communication, the composition of cumacean assemblages at the Golfo Ártabro is described according to bathymetric distribution and nature of substratum.

Recovery of deep-water megafaunal assemblages from anthropogenic disturbance in the Norwegian Sea

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Recovery from disturbance is poorly understood in deep water, but the extent of anthropogenic impacts is becoming increasingly well documented. We used Remotely Operated Vehicles (ROV) to visually assess the change in benthic habitat after exploratory hydrocarbon drilling disturbance around the Morvin well located at 380 m depth in the Norwegian Sea. An ROV, launched directly from the rig drilling the well was used to carry out video transects around the well before drilling and immediately after. On a return to the site three years after disturbance a larger survey was conducted with a ship-launched ROV. Transects were repeated at the disturbed area and random background transects were taken. Visible drill cuttings were mapped for each survey and positions and counts of epibenthic megafauna were determined, revealing a fauna dominated by Cnidaria (45% of total observations) and Porifera (33%). Immediately after disturbance a visible cuttings pile extended to over 100 m from the well and megafaunal density was significantly reduced (0.07 individuals m^{-2}) in comparison to pre-drill data (0.23 ind. m^{-2}). Three years later the visible extent of the cuttings pile had reduced in size, reaching 60 m from the well and considerably less in some headings. In comparison to background transects (0.21 ind. m^{-2}), megafaunal density was significantly reduced on the remaining cuttings (0.04 m^{-2}), but beyond the visible disturbance there was no significant difference (0.15 m^{-2}). The investigation at this site shows a return to background densities of megafaunal organisms over the majority of the area disturbed. However a central area of reduced sessile megafaunal density persists three years after disturbance.

Large-scale biogeographical patterns of Paramesochridae in South Atlantic abyssal plains and the deep Southern Ocean: is the abyssal harpacticoid copepod fauna cosmopolitan?

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Within the framework of the international project CeDAMar, the deep-sea campaigns DIVA and ANDEEP in 2000, 2002 and 2005 to the southern Atlantic Ocean (Guinea, Angola and Cape Basins) and the Southern Ocean (Weddell and Scotia Seas) yielded multicorer meiofauna samples from 21 stations. At depths down to 5655 m, a total of 437 cores were collected from 83 deployments with the multiple corer. In the present study, all 311 adult Paramesochridae Lang, 1944 (Copepoda, Harpacticoida) were analyzed at the taxonomic-morphological level. They belonged to 19 species and four genera (*Emertonia* Wilson, 1932, *Leptosyllus* T. Scott, 1894, *Paramesochra* T. Scott, 1892 and *Wellsopsyllus* Kunz, 1981). Eleven species were restricted to single regions, whereas the others showed a much wider distribution. For example, the species *E. andeep* (Veit-Köhler, 2004) and *E. diva* (Veit-Köhler, 2005) were both collected from Guinea, Angola and Weddell abyssal plains, and *E. schminkei* (Veit-Köhler & Drewes, 2009) occurred in the three West-African basins. These wide distribution ranges are unexpected as Paramesochridae are small, sediment-dwelling copepods with limited mobility and non-planktonic larvae. This study provides a first insight into the large-scale biogeography of deep-sea harpacticoids, represented by the Paramesochridae, and indicates that distribution ranges may extend across South Atlantic and Southern Ocean abyssal plains.

Prokaryotic abundance and bacterial community structures in the deep Mediterranean Sea

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The Mediterranean Sea is characterised by relatively high and constant temperatures, and an increasing gradient of oligotrophy from West to East, thus making it a unique system for study. The BIOfun project is aimed at understanding deep-sea biodiversity and ecosystem functioning. This is necessary to assess the impact of natural and anthropogenic factors and to provide management options. As part of this project, samples were taken from the water column (between 50 m and 5100 m) from the West to East of the Mediterranean (1.9°E to 34.4°E) during a number of cruises undertaken between June 2008 to November 2009. Total prokaryotic abundance was determined using epifluorescence microscopy for samples collected throughout the water column. In line with published studies, total prokaryotic counts were found to decrease with depth. A high degree of variability in abundance was found between stations but no spatially coherent pattern from West to East was apparent. Bacterial community structure was studied by means of Denaturing Gradient Gel Electrophoresis

(DGGE) analysis of PCR-amplified 16S rRNA genes. Gel images were analysed with TotalLab TL120® software to create matrices of relative OTU abundance for multivariate statistical analysis. There were great differences in community structure between some Eastern and Western stations. However a number of bands were seen to be shared between geographically distant sites. No appreciable change in bacterial diversity (Shannon's index) was found from West to East. Species richness was found to be relatively constant at all depths sampled at each individual site.

Bathymetric-zoogeographical traits of the Hexactinellida from the Antarctic deep-sea expeditions ANDEEP and SYSTCO

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Sponges were sampled during the ANDEEP-SYSTCO expeditions (2002-2008) by various benthic sampling gears, especially Agassiz trawl, epibenthic sledge and Rauschert-dredge. Taxonomic analysis was done by SEM and LM on spicule preparations. Ecologic analysis was done with several computer programs including MS excel, Past and Ocean Data View. 26 hexactinellid taxa were sampled during ANDEEP-SYSTCO-Expeditions, 7 of which were new to science. In here, we will just give a brief insight into the sponges from SYSTCO-expedition. These contain three species from the deep-sea, two of which are very widespread and characteristic in the Antarctic deep-sea, and one, which is a new species, *Lonchiphora* nov. sp., representing a rarely known genus with a remarkable distribution. Ecological analysis has shown, that three distinct associations of glass sponges can be found, replacing each other towards the depth. These are characterised by the following species: *Rossella* spp. on the shelf, *Bathydorus* spp. on the continental slope and in the shallower deep-sea and *Caulophacus* spp. in the deepest abyssal. Although there are several studies on Antarctic glass sponges, most of which are dating from the late 19th century, still few is known about the detailed distribution and ecology of these animals. The results from ANDEEP-SYSTCO show, that a number of species are still unknown and that further studies can be expected to bring a deeper insight into this field. Especially the concept of the three sponge associations with their character species is entirely new and allows a first detailed look into the ecology of Antarctic glass sponges.

Composition and structure of vestimentiferan associated assemblages from Guaymas Basin and 9°N East-Pacific Rise: comparative analysis

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The vestimentiferan tubeworms *Riftia pachyptila* form dense aggregations at hydrothermal vents on the East-Pacific Rise (EPR) and in Guaymas Basin. They occupy areas of vigorous diffuse flow, with temperature range from 2 to ~30°C and high sulfide concentration. Vestimentiferan bushes house a lot of invertebrate species. Taxonomic composition and structure of invertebrate fauna associated with vestimentiferan bushes were examined in the Guaymas Basin and 9°N EPR. Original material was collected using submersibles Mir on cruises of the RV Akademik Mstislav Keldysh in the Guaymas Basin and 9°N EPR. Tubeworm associated assemblages from Guaymas Basin were examined for the first time. Original and published quantitative data on vestimentiferan-based assemblages from 9°N EPR were summarized. Species richness was significantly lower in vestimentiferan assemblages from the Guaymas Basin than at 9°N. Species composition of associated epifauna was remarkably different at both sites. There was no significant difference in the rate of dominant family at 9°N compared to Guaymas Basin vestimentiferan-based assemblages. Diversity was lower within Guaymas assemblages than within 9°N vestimentiferan-based assemblages. The predominant taxa were different at two sites. Lepetodrilid gastropods were numerous at 9°N whereas in Guaymas Basin abundance of gastropods in vestimentiferan assemblages was low. Analysis of *Riftia pachyptila* aggregations revealed considerable differences in composition and structure of hydrothermal assemblages on the ridge and in the basin.

Community composition and trophic patterns on rocks, wood, and biotic substrates at Costa Rican methane seeps

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Methane seeps, though sometimes thought of as soft sediment habitats, contain a variety of hard substrates: authigenic carbonates, sunken wood, and biogenic substrates such as vestimentiferan tubes or mussel shells. We asked whether hard substrate identity can control community structure by comparing macrofauna on replicate deployments of carbonates, wood, worm tubes, and bivalve shells to one another and to natural hard substrates at a 1000 m methane seep off Costa Rica. We hypothesized that faunal composition and dietary patterns on experimental substrates would more closely resemble those of similar natural substrates than different types of substrate in the same location. Gastropods dominated most hard substrates, making up 45-74% of the individuals on wood, carbonate, tubeworms, and

mussels. While community structure varied among experimental substrates, spatial distance had a stronger influence on community structure, especially in terms of the abundance of dominant species (generally *Provanna* and limpets of the genera *Pyropelta*, *Lepetodrilus*, and *Paralepetopsis*). Polychaetes were less abundant than gastropods but exhibited higher diversity. Of 36 polychaete families represented, only syllids accounted for more than 5% of the total individuals on any natural substrate (17% on vestimentiferan tubes). The most abundant polychaete families were usually different on natural and experimental substrates, suggesting other factors are important in structuring this community. Isotopic analysis suggested that organisms access different food resources depending on their substrate. Mean $\delta^{13}\text{C}$ of the carbonate (-35‰) and mussel shell assemblages (-35‰) was lighter than that of fauna associated with worm tubes (-27‰) and wood (-25‰). Likewise, fauna colonizing experimental rocks had a relatively light $\delta^{13}\text{C}$ signature (-38‰) compared to wood (-31‰). Consistent differences in isotopic signatures within taxonomic groups on a single substrate suggest that co-occurring species often utilize unique food sources. Hard substrates at methane seeps act as discrete heterogeneous patches, offering a diversity of habitats and food resources that influence species diversity and composition.

Cold-water corals of the Bay of Biscay: identification of species and habitats from video and still photographs

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The need of knowledge, the development of methods and standards about habitat mapping and ecological status assessment of Vulnerable Marine Ecosystems (VMEs) are essential for managers trying to limit the negative effects of anthropogenic activities. This is enhanced by the recent raise of European and International regulations over the deep-sea. From 1996 to 2009, 9 cruises allowing 60 dives with various ROVs, submersibles and towed camera frames were conducted in canyons and open slope of the Bay of Biscay. Videos and still images were acquired along transects over a depth range of 180-2000 m. Until 2008, most of the cruises were designed for halieutic or geological purposes. Historical records and recent observations were used to produce a list of 150 cold-water coral taxa present in the Bay of Biscay and a catalog for identification of the main taxa. Associations between coral taxa and other megafaunal taxa, relations to substrate types, geofoms and depth were tested. *Lophelia pertusa* and *Madrepora oculata* make mixed reefs occurring down to 1100 m depth in association with a large variety of antipatharians, gorgonaceans and hexactinellid sponges. Rubble and areas of trawl impacts were also recognized. The stony coral *Enallopsammia rostrata* colonizes vertical cliffs around 1500 m depth. On soft bottom, different associations were encountered including pennatulid fields, like *Funiculina quadrangularis* associated with burrowing megafauna, bamboo fields with *Acanella arbuscula*, other Isididae and stalked sponges, solitary cup coral fields with *Caryophyllia* spp. and/or *Flabellum*. Other non coral VMEs were also recognized. A comparison with the habitat definitions mentioned in regulatory texts, existing classification schemes and main scientific publications in North East Atlantic was performed.

Sources and sinks in the abyss, and their consequences for deep-sea biodiversity

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Many aspects of abyssal ecosystem structure and function are strongly modulated by the quantity and quality of particulate organic carbon (POC) sinking from the surface ocean. Only a small fraction of surface-derived organic material reaches the abyssal sea floor, and these systems are thought to experience extreme food-limitation. The lack of food is likely a major structuring force in deep-sea communities. Food-limitation in parts of the abyss results in extremely low population densities, generating an Allee effect whereby reproductive success is hampered, and population growth rates can reach zero, or even negative values. These low-quality “sink” habitats are unsustainable without immigration and/or dispersal of propagules from source areas. Some suggest the abyssal seafloor constitutes a sink habitat sustained only by an influx of larval ‘refugees’ from source areas on adjacent continental slopes. This slope-abyss source-sink hypothesis has been interpreted to mean that abyssal habitats have no intrinsic value in terms of unique biodiversity. However, quantitative tests of this hypothesis have been few, and we argue that these tests have largely been inappropriate. Further, a very important aspect of the hypothesis--impacts of primary productivity on biodiversity patterns--has been largely ignored. We will examine both the depth- and productivity-related aspects of deep-sea biodiversity patterns, and present new tests of the source-sink hypothesis. We will also propose additional, more appropriate tests, and offer a re-formulation of the source-sink idea as it applies to deep-sea systems, including predictions of geographic regions and faunal groups expected to be most susceptible to source-sink dynamics.

The diversity of *Osedax* (Annelida) borings revealed by computed tomography

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Osedax worms are noted members of both deep-sea and shallow whale-fall communities because of their unusual reproductive and feeding adaptations. However little is understood about how they interact with the bones that they bore in to. These boring activities may play important ecological roles in determining the longevity of whale skeletons on the seabed and in regulating the reduction of sulphates in the bones.

Recently fossilised borings in whale bones have been ascribed to *Osedax*, however the morphology of *Osedax* borings in modern bone is poorly known. The large-scale destruction of whale bones by *Osedax* is also of taphonomic importance in reconstructing the fossil record of cetaceans themselves.

Here we reveal the morphology of borings for several *Osedax* species using micro computed tomography (CT), allowing an accurate comparison of boring behaviours between the different species. The ecological significance of these data is discussed in relation to feeding and growth. We define consistent features of *Osedax* borings and comment on the evidence for fossilised *Osedax* traces.

Colonization of mammal carcasses in the deep Atlantic Ocean: introducing the CARCACE project

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Since the discovery of hydrothermal vents in 1977, research in chemosynthetic environments has provided many surprises about life in the deep-sea. One of the most startling discoveries was the diverse and specialized fauna found at large organic falls such as whale carcasses. The sulphide and lipid-rich nature of decomposing whalebones is thought to create an habitat intermediate to that of vents and seeps, and have allowed several vent (or seep)/whale conspecifics to use large organic falls as dispersal stepping-stones over evolutionary or ecological time-scales. In the last 10 years detailed ecological and phylogenetic studies have been carried on whale falls and several in situ experiments have been set. Surprisingly, all deep-sea and long-term studies have been restricted to the Pacific Ocean. With the CARCACE project we propose to study the community response to intense pulses of organic falls and their importance as sulphide-rich habitat islands at the Atlantic Ocean deep-sea floor. Two mammal carcasses will be deployed in two sites where cetaceans naturally occur, the Setúbal canyon (West Portuguese margin) and the São Jorge Channel (Azores) at approximately 1000 m. These experiments will allow comparing the colonization dynamics and species composition between areas with different geological and hydrological settings and address questions related to species distribution, dispersal strategies and phylogeography. Each of the experimental sites will be surveyed and sampled every six months during two years. The project is organised in five tasks that correspond to five main objectives: 1) to describe deep water mammal carcasses fauna in the Atlantic, 2) to investigate functional anatomy of organic-fall specialists, 3) to determine phylogenetic relationships of organic-fall specialists, 4) to analyse the trophic structure of colonizing metazoan assemblages 5) to elucidate the importance of large organic falls as a stepping-stone habitat for vent and seep species in the Atlantic. A sixth task will be dedicated to public outreach and education.

Reproductive ecology of deep-ocean fish

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Histological analyses were used to study the reproductive ecology of 5 species of deep-ocean fish from the mid-Atlantic Ridge (*Antimora rostrata*, *Coryphaenoides armatus*, *Coryphaenoides brevibarbis*, *Halosaurus machrochir* and *Histiobranchus bathybius*). Inter-specific variation in spawning pattern and rate of maturity was apparent although most individuals recovered were immature or maturing females. *H. bathybius* was the exception with one mature female and one immature male observed. The female had a potential fecundity of 61 307 eggs. Very little reproductive data is available for deep-ocean fish however knowledge regarding this life history trait is important for understanding the overall ecology of these species. This is particularly significant considering the continued encroachment of commercial fishing activities into deeper waters.

Metazoan meiofauna in the Gollum Channel system and on the edge of the Whittard Canyon, Celtic Margin – how the environment shapes nematode structure and function, including notes on two new nematode species associated with ecto- and endosymbiotic prokaryotes

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Within the framework of the EC FP6 HERMES project, samples were taken at ca. 700 and 1000 m depth in the Gollum Channel System and the edge of the Whittard Canyon during the RV Belgica 2006/13 cruise. These two areas are expected to receive high input of organic matter and phytodetritus, but are typified by different trophic and hydrodynamic conditions. Selected biogeochemical variables of the sediments were analysed in conjunction with structural and functional diversity of nematodes, the numerically dominant group within the meiofauna. The Gollum channels and Whittard Canyon edge were characterised by relatively high meiofauna abundance (1054 – 1426 ind. 10 cm²) and very high nematode genus diversity (total of 181 genera). The nematode community contrasted between the two study areas, between water depths and between individual sampling stations. Sediment layer differences had the largest impact on nematode community structure, indicating that local vertical sediment gradients were more important than other spatial contrasts. In addition, nematode biomass varied between areas and stations and reflected differences in trophic structure induced by local trophic conditions. For the first time, the “chemosynthetic” genus *Parastomonema* (new *Parastomonema* sp., Order Monhysterida, Family Siphonaimidae) has been found in deep-sea sediments. This genus lacks a mouth, buccal cavity and pharynx and possesses a rudimentary gut containing internal, symbiotic prokaryotes which have been recognised as sulphur-oxidising bacteria. Together with the presence of a new nematode

species associated with ectosymbiotic bacteria (*Eubostrichus* sp., order Desmodorida, family Desmodoridae, subfamily, Stilbonematinae), this may indicate the presence of a reduced environment in these canyon systems which is partially confirmed by the biogeochemical environment.

EU FP7 project DEEPFISHMAN Management and monitoring of deep-sea fishes and stocks

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DEEPFISHMAN is a research project funded by the European Union FP7. Its main focus will be on developing a range of strategy options for the exploitation of deep-water species in NE Atlantic. DEEPFISHMAN relies upon interdisciplinary research from fishery science, ecology and socio-economy. It will establish strong involvement of stakeholders in the definition of monitoring and management frameworks for deepwater fisheries. It comprises thirteen partners from nine countries.

Biodiversity and ecosystem functioning in the megabenthic community at Galicia Bank, Iberian margin

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Continental margins represent ~15% of the seafloor and provide important ecosystem services e.g. burial of organic carbon, CO₂ sequestration. CMs are also areas with high species diversity and maxima often occur mid-slope. One of the key factors influencing species diversity across CMs is food supply. Phytoplankton blooms provide the sole source of energy viz. particulate fluxes to the majority of deep-sea benthic communities. These communities are reliant on biogenic fluxes for growth, reproduction and recruitment. The biochemistry of certain fauna e.g. holothurians have been shown to reflect food supply via processes such as

selective feeding and assimilation. Similarly benthic fauna have been shown to impact their environment through both of the aforementioned processes, bioturbation and locomotion. In this study we will characterize megabenthic biodiversity across a depth gradient (1200 to 3000 m) on the Iberian margin and attempt to unravel the link between biodiversity and food supply. Abundance, biomass of megafauna will be ascertained from video surveys and Agassiz trawls. A suite of biochemical data (organic carbon, lipids, stable isotopes and pigments) will determine food quantity and quality at each of the stations. Multivariate statistics will ascertain if there is a link between food supply and biodiversity at these sites. Faunal feeding preferences will be assessed using lipid biomarkers and stable isotope analyses; trophic diversity will be assessed using a suite of indices (Layman et al. 2007).

Strong genetic divergence along a bathymetric gradient - population divergence or cryptic speciation?

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Protobranch bivalves of the Northwest Atlantic below continental shelf depths tend to be genetically structured by depth. Mitochondrial DNA (mtDNA) fragments obtained from formalin-preserved material has shown in several cases that populations of upper bathyal species exhibit strong population structure, while populations of lower bathyal and abyssal species show much less differentiation. Previous mtDNA data from populations of *Deminucula atacellana* that spanned the upper and lower bathyal (1100-3800 m) revealed two well-defined clades, with a sharp boundary inferred somewhere between 2500 and 3300 m. It was unclear whether the strong genetic divergence between upper and lower bathyal samples represented cryptic species or a single species with pronounced bathymetric variation. In 2008 we collected *Deminucula atacellana* from the North American continental slope and rise, and preserved them for molecular analyses. To test whether the pronounced bathymetric divergence represented one or multiple species, we sequenced several mitochondrial and nuclear loci from upper and lower bathyal samples of *Deminucula atacellana*. Population genetic analysis of mitochondrial COI and 16S indicated strong bathymetric divergence between upper and lower populations, but significant haplotype sharing within each zone. In contrast, nuclear intron loci showed strong genetic overlap among all populations. Nuclear ribosomal sequences revealed extremely low, but fixed, polymorphism between the upper and lower bathyal. Taken together, these results imply incipient speciation along a depth gradient for *Deminucula atacellana*.

***Bathydorus* sp. nov. and *Docosaccus* sp. nov. (Lyssacinosa, Hexactinellida): Two new species of glass sponges from the abyssal Northeast Pacific**

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Two new species of glass sponges are described from Station M, a long-term study site in the abyssal plain of the northeast Pacific Ocean. Though similar in their plate-like gross morphology, analysis of spicules from these two species places them in two different families within Order Lyssacinosa. *Bathydorus* sp. nov. (Family Rossellidae) is supported by evenly-spaced lophophytous spicules that project into the soft sediments of the abyssal plain. Its perimeter is lined with long spicules, giving it a hairy appearance. The species is white to cream color and has no visible oscula on the upward-facing atrial surface. Spicules include long, blunt-tipped diactins, smooth pentactins, spiny stauractins and hexactins. Microscleres include hexasters, hexactins, and oxyhexasters. Within the genus, the new *Bathydorus* species does not match any of the existing eight species based on its biogeography and the spicules that comprise its skeleton. *Docosaccus* sp. nov. (Family Euplectellidae) also has long lophophytous spicules that anchor it into soft sediments, but they project in tufts from the bottom of the sponge and are not present along its perimeter. Visible oscula on the atrial surface give individuals a spotted appearance. Spicule analysis places the sponge into Family Euplectellidae and its lophophytous method of attachment places it in Subfamily Euplectellinae. Megascleres include hexactins, pentactins, and diactins; microscleres include oxyhexasters, hemioxyhexasters, and floricoles. The presence of extremely large hexactins eliminates most genera within Subfamily Euplectellinae, leaving the monospecific genus *Docosaccus* Topsent 1910. Descriptions of these new species are necessary as studies will soon emerge establishing sequences of their mitochondrial genomes and studying population-level changes using time-series data from Station M.

Investigation of cold water coral ecosystems of the Azores archipelago within the framework of EU FP7 project CoralFISH

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Evaluation of the effectiveness of closed areas as a conservation management practise is dependent upon the development of monitoring tools and the collation of baseline data which at present are often lacking from deep waters around Europe. The integration of fish into coral ecosystem models to better understand the interaction between cold-water coral habitat, fish and fisheries, and to help develop such monitoring and predictive modelling tools for ecosystem-based management is one objective of the EU CoralFISH project (FP7, Theme 6). In addition the investigation of settlement behaviour and life history of specific coral species,

and the use of molecular tools to establish patterns of connectivity between coral populations enables us to describe dispersal patterns and consequent resilience or vulnerability of such deep-water coral ecosystems. Work towards achieving these two objectives has been undertaken in the Azores region with the use of a manned submersible utilised to collect HD video surveys of cold water coral garden ecosystems, and to collect samples for genetic analysis. Settlement panels placed on the seafloor for periods of 1 and 2 years form the basis of investigations into the life history and settlement patterns of representative epifaunal species. The development of these methodologies and the collation of baseline survey data is described.

Isolation and characterization of sulfate reducing bacteria (SRB) from wood falls

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Anaerobic microorganisms involved in the reduction of sulfur compounds, and sulfate-reducing bacteria (SRB) in particular are known as significant contributors to the oxidation of organic matter in marine environments. In this respect, enrichments from wood falls sampled during the Medeco cruise in November 2007 and in the Gulf of Cadiz (Atlantic Ocean) in 2008 have been performed to look for SRB inhabiting such ecological niches. They allowed us to isolate from Mediterranean Sea (1700 m depth) two novel strains of SRB: strain C1TLV30, considered as a novel bacterial species (*Desulfovibrio piezophilus*), having 96% similarity with *D. profundus*, a piezophilic hydrogenotrophic SRB isolated from deep-sea sediments and strain C1TH30 having 99% similarity with *D. dechloracetivorans*, an acetoclastic SRB also isolated from marine environments. Further enrichments from the Gulf of Cadiz samples (354 m depth) led to the isolation of two other SRB : strain B0109P2, having 98% similarity with *D. dechloracetivorans*, and strain B0109G, having 98% similarity with *D. marinisediminis*. Both isolates should be also considered as novel species of genus *Desulfovibrio*. Among them, strain C1TLV30 was already shown to be piezophilic growing optimally at 100 bars and up to 250 bars. Isolation of hydrogenotrophic and acetoclastic *Desulfovibrio* strains from wood fall samples at different depths in the Mediterranean Sea and in the Atlantic Ocean suggest that these microorganisms should be considered of ecological significance in the decomposition of wood falls in deep marine environments

Three new species of *Cerviniella* Smirnov, 1946 (Copepoda: Harpacticoida) from the Arctic

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Considered one of the most common harpacticoid families in deep sea benthos, the Aegisthidae can be found in various marine sediments and at different depths. During the fourth leg of the ninth expedition of RV Polarstern into the Arctic Ocean (ARK-IX/4) in 09/1993, three new representatives of the genus *Cerviniella* were collected in multicorer samples from the Laptev Sea at a depth of 760-2017m. Although this genus had already been record from the Arctic Ocean by Smirnov (1946), the present research raises the number of species known for the region from 1 to 4, and to 11 worldwide. *Cerviniella* sp. nov. 01 and 03 can be easily distinguished from their congeners primarily by the segmentation of the antennules, maxilla and leg 4, and setation of legs 1-5. *Cerviniella* sp. nov. 02 differs from the other species by the following combination of characters: shape of the rostrum and armature of leg 1 and leg 3 endopods. The study of adults and copepodites also provided significant information about the development and morphological adaptation of the swimming legs in this group. This study was supported by the Census of Marine Life project “Arctic Ocean Diversity” www.arcodiv.org

***Pontostratiotes* Brady, 1883 (Copepoda: Harpacticoida) from Angola deep-sea basin (Southeast Atlantic, DIVA 1)**

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Pontostratiotes constitutes the most specious genus in Aegisthidae and a common presence in the deep sea benthos. Twenty six species can be found in the Atlantic, Pacific and Indian oceans, in various sediments and at depths ranging from 920 to 5590 m. During the first leg (METEOR 48/1) of the project DIVA (Latitudinal gradients of Deep Sea BioDiversity in the Atlantic Ocean), samples were taken in 6 areas along a transect of about 700 km crossing the southern part of the Angola Basin, in July and August of 2000. A total of 143 adult specimens of *Pontostratiotes* were sampled with epibenthic sledges at depths between 5117 and 5455m, revealing 8 new species that can be clearly distinguished from the other known species of this genus mainly by the dorsal processes that ornament the prosome. Other minor differences in the first antennular segment, armature of the P5 and morphology of the caudal rami were also observed. The most abundant species was *Pontostratiotes* sp. nov. 6, dominant in the North part, followed by 3 species (*P.* sp. nov. 1, 2 and 3) those occurred in both extremes of

the transect. Three other species (*P. sp. nov.* 5, 7 and 8) were restricted to single areas and were poorly represented. This study was supported by the Census of Diversity of Abyssal Marine Life (CeDAMar).

Spatial changes in community structure of harpacticoids around trenches

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Trenches are developed at subduction boundaries and reach 6,000-11,000 m depth. If depth is sufficient barrier to the expansion of animals, it is expected that there are endemic animals at trenches. In fact, about 60% species and 10-25% genera of large benthic animals at trenches are endemic (cf. Angel 1982). Knowledge of community structure of meiofauna around trenches is still limited, although the organisms exceed large animals in density and biomass, and are important components in deep sea ecosystem. We studied spatial changes in community structure of harpacticoids (Crustacea: Copepoda) around the Ryukyu Trench and the Kuril Trench at genus level. Sampling at the Ryukyu Trench Region (12 stations) and the Kuril Trench Region (8 stations) were conducted at May 2005 and September 2001, respectively, using a multiple corer. Sampling stations were established along transects from continental slopes to abyssal basins, crossing trenches. There was no genus that seemed new to science and was found only at trench stations, suggesting that endemic genera are rare in the two trenches. Multivariate analysis revealed that the community structure of harpacticoid assemblages at the trench stations was more similar to that of the continental slopes than that of the basins at each trench area. Furthermore, comparisons between the two areas showed that the similarities in community structure between the trenches and the basins were lower than that between the slopes. These results suggested that harpacticoid genera diverged and expanded their distribution ranges in continental margin, and then expanded to basins through trenches.

Amoebozoa in deep-sea samples from the western Atlantic revealed by the DIVA3 expedition on board RV METEOR

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Though heterotrophic protists are an important component of marine benthic and pelagic communities, their diversity on the sea bottom that represents the world's largest habitat, is still poorly known. Certain progress in the characterization of the deep-sea protists has been

made during recent years, but this was mostly focused on specific groups like heterotrophic flagellates or foraminiferans. Lobose amoebae (phylum Amoebozoa) may play an important ecological role in shallow and freshwater ecosystems, however, they remain virtually unknown from the deep-sea. Due to their properties, living amoebae are often overlooked in the fresh benthic samples, and remain undetected in the environmental clone libraries. We attempted to fill this gap by looking for cultivable amoebae species in the deep-sea sediment samples (ca. 3800-5200 m deep) collected from the Argentine and Brasil abyssal plains (western Atlantic) during the cruise M79/1 of the German research vessel Meteor in July-August 2009. Altogether about 20 strains of marine amoebozoans have been isolated. Out of them, 16 strains representing 9 morphospecies could be brought into a stable prolonged culture allowing an extensive study and identification using morphological and molecular genetic tools. Most of these strains (11) belong to the family Vannellidae and comprise four morphospecies (several morphospecies were represented by multiple strains isolated from different samples), including one deeply-branching vannellid amoeba (probably member of a new genus) and three new species of *Vannella*. Other species belong to the Dactylopodida (*Neoparamoeba* sp.; two new species of Vexilliferidae and Paramoebidae), Cochliopodiidae (a new species probably representing new genus) and Variosea. Comparison of the *Vannella* strains using morphological and molecular genetic markers (nuclear small-subunit ribosomal RNA and mitochondrial cytochrome C oxidase genes) shows that two out of the three morphospecies found are represented by two distinct genotypes each. This study has been supported by the DFG grant HA 818/22-1.

Hydrothermal seeps: the best of both worlds

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Hydrothermal vents and methane seeps have long been considered distinct environments that share chemosynthetic genera with linked evolutionary histories. At the base of a collapsed seamount within the Costa Rica subduction zone we discovered warm, methane-rich diffuse flow fueling a novel hybrid vent-seep ecosystem. At this site (Jaco Scarp, 1792 m), mildly warm (3.2 to 5.2°C), shimmering fluids were emanating from beneath several large *Lamellibrachia* bushes, with ambient waters at 2.6°C. *Lamellibrachia* aff. *barhami* occurred in large, volkswagen-sized bushes and in continuous fields along steep topography. The tubeworm bushes subject to diffuse flow supported bathymodiolin mussels and *Thermarces*-like zoarcids between tubes, with dense *Lepetodrilus* populations and bacterial mats covering

the tube and mussel shell surfaces bathed in flow. Dense assemblages of large vesicomimid clams covered with *Cataegis* (Gastropoda) and galatheid crabs surrounded the hydrothermally active bushes. Fields of frenulate polychaetes and bacterial mats with massive numbers of *Ophiura* occurred beyond these. Other tubeworm bushes, not exposed to obvious hydrothermal activity, were covered with large serpulids (*Laminatubus* sp.) and sabellid polychaetes. The assemblages are marked by exceptionally high biomass, with appearance more closely resembling the Juan de Fuca/Endeavor system than those of most sediment- or carbonate-hosted methane seeps. The mussel, ophiuroids, galatheids, zoarcids, and some gastropods appear to have hydrothermal vent affinities. The foundation species (*Lamellibrachia*, *Escarpia*, vesicomiyids, frenulates) and their associated polychaetes appear to be seep genera; molecular confirmation is pending. Isotopic analyses suggest this hybrid system is fueled largely by sulfide oxidation, with serpulid, nereid, ampharetid, and hesionid polychaetes and a lepetopsid gastropod reliant on methane. The modes of co-existence of different species at this site informs our understanding of the evolution of vent and seep ecosystems and the ecological and environmental 'rules' which govern modern chemosynthetic systems.

Scotopic optical sensitivity in Chondrichthyes

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The role of scotopic optical sensitivity in a range of Chondrichthyes is examined. This is a group of species that occupy a variety of different habitats ranging from shallow waters to abyssal depths of ca. 3,500 m, some 2,500 m beyond the penetration of sunlight. In addition, some Chondrichthyes may guide themselves across a wide range of depths, stretching their distribution several hundred meters in the water column. Taking into account that within the mesopelagic zone (200 to 1000 m) daylight intensities vary by more than 13 log units and disappear completely by 1000 m, these fishes are a useful group for comparing interspecific variation in scotopic optical sensitivity with changes in environmental light intensity. Scotopic optical sensitivity was examined by analysing the anatomical parameters implied in improving light absorption i.e. the pupil aperture, the solid angle of visual space each photoreceptor perceives and the fraction of incident light each photoreceptor absorbs. Twenty-two species (18 sharks, 3 skates and 1 chimaera) with different lifestyles and inhabiting different parts of the water column were chosen to highlight interspecific differences in enhancing sensitivity. Here we hypothesise that, in Chondrichthyes, scotopic optical sensitivity increases with habitat depth. The analysis leads to the conclusion that a progressive improve in optical sensitivity was correlated with an increase in habitat depth, but only in Chondrichthyes species distributed above the mesopelagic zone. Instead, for species whose depth distribution reached and went through the bathypelagic zone, optical sensitivity decreased dramatically. The ecological significance of these results is discussed in relation with Chondrichthyes predatory behaviour and the changing nature of visual scene with depth.

Distribution of deep-sea corals in the Makapu'u coral bed, Hawaii, and temporal changes in crinoid abundance

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Deep-sea coral communities provide three-dimensional, spatially-complex habitat to diverse populations of benthic organisms, as well as serving as paleoclimatological and paleoceanographic proxies. High levels of endemism among coral-associated fauna have been reported, especially in conjunction with seamounts. With their fragile and sessile lifestyle, deep corals are thought to be especially threatened by destructive fishing practices and the anthropogenic alteration of seawater chemistry. Currently, little is known regarding distributions of deep-sea coral populations, particularly at local scales. The Makapu'u precious coral bed ranges in depth from 375-450 meters and covers an area of approximately 3.6 square km offshore of the island of Oahu, Hawaii. In this ongoing study, video analysis and GIS techniques are coupled to map deep-sea coral occurrence and community composition. Substrate composition, and where available, salinity and temperature data, are related to coral occurrence and composition. The ROV and submersible video data utilized, made available by the Hawaiian Undersea Research Laboratory (HURL), cover a broad time-series (1981-present) at this site, allowing for investigation of temporal changes in crinoid abundance.

Dwelling in the deep: population structure and habitat use in the deep-sea macrourid *Coryphaenoides rupestris*

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The patterns of spatial structuring in deep sea species represents one of the next frontiers in marine biology. Here we investigated population connectivity and habitat use in the deep-sea macrourid *Coryphaenoides rupestris* collected in different areas in the North Atlantic, using a suite of chemical approaches. Otolith microchemistry, based on Laser Ablation/ICP-MS from primordium to otolith edge, found significant differences in the concentrations of Li/Ca, Mn/Ca and Ba/Ca among sample sites for *C. rupestris*. This allowed for very high classification accuracy (92%), when using discriminant function analysis, suggesting strong stock structure of *C. rupestris* in the North Atlantic. Using otolith $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ stable isotopes, the metabolic activity and estimated depth inhabited by *C. rupestris* was examined (using a temperature equation modified for all deep-sea fish). Compared to other macrourids, metabolic activity in *C. rupestris* was found to be relatively high, consistent with the more pelagic nature of its diet. However metabolic activity was found to decrease significantly over the lifetime of the fish. $\delta^{18}\text{O}$ values suggest that *C. rupestris* inhabits shallower waters in early life and consistently migrates deeper with age. By comparing the microchemistry of the

otolith from larvae to adult, in addition to the isotopic analysis of the otolith, we are able to reveal stock structure in a poorly-known exploited species and contribute to the challenge of exploring life in the deep sea.

Life history of a long dark fish in a deep dark Ocean: *Aphanopus carbo* in the North Atlantic

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The study of the chemical characteristics of otoliths is quickly establishing itself as a fundamental tool in fish stock identification. Using a dual approach of otolith microchemistry and otolith isotope analysis, the stock structure and life-history of the deep-sea trichiurid *Aphanopus carbo*, collected in different areas in the North Atlantic, were examined. High definition microchemical analyses revealed a high degree of overlap among samples from areas as distinct as the Azorean Mid-Atlantic Ridge and the Rockall Trough. Combining microchemical information with data on life-history traits in different areas, we suggest that *A. carbo* may exhibit a strong and extensive migratory behaviour, exploiting certain areas in the North Atlantic for spawning and others for feeding. Stable Carbon Isotope Analysis suggests that *A. carbo* is considerably more active than other deep-sea fish, possibly reflecting a greater degree of pelagic predation and migratory behaviour. The life-history of *A. carbo* is further discussed in light of both Oxygen and Carbon stable isotopes, and collective evidence adds a glimpse of understanding to the fascinating ecological dynamics of the least known habitat on the planet. By comparing the microchemistry of the otolith from larvae to adult, in addition to the isotopic analysis of the otolith, we unveil patterns of life-history that can contribute to the understanding of the deep sea ecosystem.

Deep-sea syllids (Annelida: Polychaeta) from ‘DIVA-Artabria I’ project (2002 expedition) in the continental shelf and upper slope off Galicia (NW Spain)

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The results of the study of 1181 individuals of the family Syllidae (Annelida, Polychaeta) from ‘DIVA-Artabria I’ project (2002 expedition) are presented in this communication. The family Syllidae Grube, 1850 comprises one of the most diverse and well-known groups of polychaetes inhabiting hard and soft littoral marine bottoms. Knowledge on syllids from many areas of the world, including the deep sea, is still scarce. In 2002, the Marine Biological Station of A Graña (Universidade de Santiago de Compostela, Spain) started the ‘DIVA-

Artabria I' project as a survey of the benthic fauna of the Galician shelf and slope off Golfo Ártabro (NW Spain) in order to obtain baseline data about diversity, composition and distribution of benthic assemblages. Sampling stations were located along a transect starting at depths of 150 m in the continental shelf and crossing the continental slope in NW direction to depths of about 1,000 m. Three different sampling gears were deployed depending on the nature of the substratum: Agassiz Trawl, Naturalist dredge and Epibenthic sledge. Sandy-muddy sediments are present at the continental shelf while the slope is characterized by hard substrata such as stones, corals and carbonated formations. In this poster, data on distribution and composition of syllid assemblages according to bathymetry and nature of substrate are presented. Analyses revealed that syllids are more abundant and diverse at deeper, hard-bottom stations than at shallower, soft-bottom stations.

A new genus and species of Syllidae (Annelida: Polychaeta) from deep-sea areas off Norway with unusual morphological characters and uncertain systematic position

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In this poster, the description of a new enigmatic genus and species of Syllidae (Polychaeta), from deep-sea areas off Norway, is given. Material examined comes from benthic samples taken at depths of between 330 and 379 m deep, at a number of oil platforms off Norway. Body appearance of the two only specimens available looks unusual for a syllid but a typical pharynx and proventricle are present. These specimens are characterized by lacking palps, eyes, and median antenna, having a single pair of peristomial cirri, distinct ventral cirri fused all along their length, two parapodial lobes, a slender, coiled pharynx without trepan but with a pharyngeal tooth, and compound chaetae with long shafts, distally enlarged and spinose, and long, filiform blades, quite similar to those of the members of the family Phyllodocidae. These very unusual characters are unique among the syllids and grant the creation of a new genus for those specimens. Some characters indicate certain affinities with the syllid subfamily Autolytinae but their truly position within the Syllidae could not be ascertained until more material are available for further phylogenetic analyses.

Low Aragonite Saturation States Surrounding Deepwater Coral Communities in the Northern Gulf of Mexico

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Existing models of deepwater calcium carbonate saturation states lack data from the Gulf of Mexico. This paucity of data should not be overlooked as the deep waters of this region harbor cold-water coral communities, including several structured by scleractinians such as

Lophelia pertusa. During a recent cruise to the Gulf of Mexico, we collected bottom water samples using the ROV Jason II and a CTD rosette. We measured pH and alkalinity and determined the aragonite saturation state (Ω_{arag}) for each sample. Aragonite saturation states were less than 1.0 at sites of moderate to high *L. pertusa* abundance. In contrast, we found saturation states greater than 1.0 localized over a cold-water coral carbonate mound at Viosca Knoll 906. The live coral on this mound had a significantly denser skeleton than corals sampled from other sites where Ω_{arag} was less than 1.0. These data contribute to our understanding of *L. pertusa* calcification and the potential impacts of ocean acidification on deep-sea coral communities.

Microbial diversity of the Grímsey high-temperature vent field on the subpolar Mid-Atlantic Ridge

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The microbial diversity of the unique, recently discovered high-temperature vent field east of Grímsey, North of Iceland, was examined by *in situ* colonization experiments and molecular analysis of the biomass obtained therefrom. Two *in situ* colonization supports were deployed at 394 m within the upper layers of a sediment-rich vent field over 53 h, in a zone of percolating 50 to 80°C NaCl-impoverished hydrothermal fluid. 16S rRNA sequence analysis indicated that a majority of putatively hyperthermophilic, thermophilic and moderately thermophilic *Bacteria* (53 phylotypes) and *Archaea* (14 phylotypes) were recovered, scattering through several taxonomical divisions. The most abundant clones in the *Bacteria* libraries belonged to the ϵ -*Proteobacteria* (36 phylotypes, 84% of 219 clones) followed by clones corresponding to other subclasses of the *Proteobacteria*, to *Bacteroidetes*, *Actinobacteria*, *Deinococcus-Thermus*, *Firmicutes*, *Desulfurobacterium* and *Coprothermobacter* groups and *Aquificae*. One colonizing support was supplied with 0.25% yeast extract and tryptone in order to promote the *in situ* enrichment of heterotrophs and supported the growth of 16 out of 17 non- ϵ -proteobacterial bacterial phylotypes. The *Archaea* were dominated by members of the *Thermococcales* (9 phylotypes, 91% of 102 clones) followed by few phylotypes belonging to the *Archaeoglobales*, *Thermoproteales*, uncultured *Crenarchaeota* and *Korarchaeota*. The 16S rRNA genes of three *Thermus* species were amplified by means of PCR, which is, to our knowledge, the first instance of amplification of *Thermus* spp. DNA directly from biomass originating from hydrothermal vents. High sequence dissimilarity was observed in the ϵ -proteobacterial populations and new putative novel lineages were detected, suggesting that distinct geographical species isolation may have occurred. This study constitutes the first report on the analysis of the microbial diversity from hydrothermal vents of the Mid-Atlantic Ridge localized beyond the Arctic Circle.

Colonization of artificial substrates in mud volcanoes from the Gulf of Cadiz – macrofauna assemblages

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The CHEMECO project (Monitoring colonisation processes in chemosynthetic ecosystems) involves a multidisciplinary study of colonisation processes in different reducing habitats from European deep-waters. The Gulf of Cadiz, one of the selected areas for this study, encompasses a number of mud volcanoes, with diverse geological settings, which have been the focus of geological and ecological surveys in the last years. The biodiversity of the recruited metazoan communities with particular attention to polychaete and bivalve symbiotic species are being analysed. The study includes a combination of site surveys and replicate colonization experiments (CHEMECOLI) using organic (wood and alfalfa grass) and inorganic (carbonate) substrata. Sets of CHEMECOLI, each with one of the three substrata, were deployed in four mud volcanoes along a depth gradient: Mercator (350 m), Mekkès (700 m), Darwin (1100 m) and Carlos Ribeiro (2200 m). In Mercator three sets were deployed in order to illustrate temporal variations of the assemblages. Up to now, two sets from Mercator and the ones from Mekkès and Darwin were already recovered and are currently being processed. The immersion times range from 10 months to two years. The macrofauna assemblages show important variations with the substrate type, and immersion time. In the carbonate samples no conspicuous animals were found while in alfalfa grass amphipods and polychaetes are the most abundant groups and the wood experiments are densely colonised by wood-boring bivalves. The biodiversity, taxonomic composition and community structure of the assemblages is described and compared to the natural background fauna.

Video quantitative survey of western mediterranean open slope communities by ROV (Remote Operated Vehicle)

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ICM (SPAIN)
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The diversity and abundance of species between 450 and 800 m depth along the Valencia Trough (Western Mediterranean Sea) were quantified after the analysis of digital videos acquired with a ROV. A variety of bottom types and geological structures was observed (i.e., soft sediment, rock outcrops, a seamount, ridges, morphological steps and cracks). While 9 phyla were identified annotated, taxonomical determination could be carried out for several individuals down to the species level. We found a general and progressive increment of diversity and species abundance when approaching the seamount, which could be then defined as a 'hot spot'. Also diversity and abundance increase as depth decreased. Tubular

polychaeta and macrourid fishes were more abundant over muddy bottoms at greater depths. In return, crustacean, cnidarians and sponges dominated in the seamount and at shallower depths. Results are discussed in terms of community zonation and seascape ecology as function of the depth and the presence of seamount structures. Technological limitations of ROV videos surveys in the deep-sea are also discussed and compared to other more traditional methods for biodiversity estimation such as, for example, scientific trawling.

Taxonomical composition and seasonal differences of megabenthic and benthopelagic invertebrates (non-crustaceans) in western mediterranean open slope and canyon

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The bathyal megabenthic invertebrate community (excluding crustacean and polychaeta) is to date still poorly described in the deep continental margins of the Mediterranean Sea. The present study tries to characterize the taxonomy and the distribution of those heterogeneous taxonomical groups along the different season of a year period. For that purpose, two different areas of the Catalan continental margin (Western Mediterranean) were targeted: Blanes open slope and the local canyon. Sampling for community characterization was carried with two different sampling gears, an otter trawl equipped with a cod-end mesh (12 mm square mesh, OTMS) and an Agassiz trawl (same mesh size = 12 mm.), in four oceanographic cruises at different year seasons (February, May, September, and November). Five depths strata were considered for the open slope (900, 1050, 1200, 1350, and 1500 m) while for the canyon, sampling depths were two (i.e. 900 and 1500 m, because the geomorphologic difficulty of trawling in the canyon axis). Thirty six species in 7 phyla were collected. Several species like heart urchin (*Brissopsis lyrifera*), and some gasteropoda like *Trophon echinatus*, or *Euspira fusca* are 'quasi' exclusive of canyon habitat. Asteroidea, Holothuroidea and Cephalopoda are predominant on open slope though in canyon; the class Gastropoda is more represented in terms of number of collected species. Present results are discussed.

Reproductive biology, including spawning periodicity and development, of the deep-sea scleractinian coral *Flabellum angulare*

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Deep-sea scleractinian corals *Flabellum angulare* were collected from the northwest Atlantic at depths of 600-1450 m to investigate their reproductive biology and periodicity using preserved and live individuals. Gametogenesis was synchronous among males and females collected from the same geographical area and depth. However, gametogenic stages and oocyte size frequency distributions fluctuated seasonally over the annual cycle. Evidence of

gamete synthesis first appeared in January-February in both sexes. Analysis of preserved samples by micro-surgery and histology combined to the monitoring of live individuals kept in a mesocosm showed that broadcast spawning occurred in May-June. Observation of contacts among conspecifics of the opposite sex just before the reproductive period suggests that they may serve in mediating reproductive synchrony. Gamete release in males and females coincided with rising seawater temperatures and high sedimentation rates indicative of seawater productivity. Oocytes (ca. 1200 μm) were released through the oral cavity. Generally, bundles of 3-5 oocytes surrounded by acontia fragments were attached to a mucus filament (3-5 cm long). Ovulation occurred in the water column followed immediately by fertilization. Oocytes that became free initially remained in the tentacles of the spawner before falling onto the surrounding substratum. The lecithotrophic embryos developed into planula larvae measuring 5-7 mm long in about 24 h.

Evidence of dietary feedback in a facultative association between deep-sea gastropods and sea anemones

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The diets of epibiotic sea anemones *Allantactis parasitica* and their gastropod hosts were analyzed using digestive tract contents, lipid biomarkers and observations of live specimens in an attempt to detect dietary feedback from the facultative association. Comparisons were made using symbiotic individuals (78 gastropods carrying 126 *A. parasitica*) and asymbiotic counterparts (18 *A. parasitica* living on inert substrata and 10 gastropods devoid of epibionts) collected at depths of 191-627 m from three distinct areas in the northwest Atlantic. Gastropods carrying one or two epibionts had higher stomach indices than those harbouring three epibionts or no epibiont. The diet of symbiotic gastropods was also more diversified based on stomach contents and lipid analysis. Among other things, symbiotic gastropods contained four times more lipids and a greater proportion of $\Sigma n-3$ fatty acids. Gastrovascular content indices of asymbiotic sea anemones were generally lower than those of symbiotic counterparts. Their cavities were more often empty, and their diet less diversified with fewer benthic items, suggesting that foraging of gastropods through the sediments makes more food available to sea anemones living as epibionts. Lipid analysis showed some disparities between symbiotic and asymbiotic sea anemones at the regional scale, including in percent phospholipids and in the proportion of certain fatty acids. Together these findings indicate that mutual protection against predators leads to prolonged and more efficient foraging for gastropods and increased time spent deployed (feeding) in food-rich areas for sea anemones, thus enabling both partners to fully exploit food resources that may be limited at bathyal depths.

Distribution and composition of deep-sea echinoderm assemblages (Holothuroidea, Echinoidea and Ophiuroidea) along a bathymetric transect off Golfo Ártabro (Galicia, NW Iberian Peninsula)

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In this communication, preliminary results on distribution and composition of echinoderm assemblages (Holothuroidea, Echinoidea and Ophiuroidea) from bathyal depths at the continental shelf and slope off Golfo Ártabro NW Iberian Peninsula) are presented. Samples were collected during the "DIVA – Artabria I" expedition in September 2002 on board the R/V Mytilus, along a bathymetric transect of depths of between 150 and 1150 m. Three different sampling gears were used: Agassiz trawl, Naturalist dredge and a modified Epibenthic sledge. Material collected included both poorly known species and others scarcely found at the studied depths. Although some taxa were distributed along all depths, multivariate analyses distinguished two different echinoderm assemblages. The first assemblage was composed by some species found at sandy-muddy sediments at the continental shelf, at depths of between of 150-400 m; the second assemblage was distributed along the continental slope, in hard bottoms (stones, carbonated structures, corals) at 600-1000 m depth.

Polychaetes from the continental shelf and upper slope off Golfo Ártabro (NW Spain). Results of the ‘Diva-Artabria’ 2002 and 2003 expeditions

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The composition and distribution of polychaete faunas from the continental shelf and slope remain poorly known. The Marine Biological Station of A Graña (EBMG-USC, Spain) started in 2002 the ‘DIVA-Artabria’ project as a survey of the Galician shelf and slope benthic fauna off the Golfo Ártabro (NW Spain) in order to obtain baseline data about benthic fauna. In this communication, the composition and distribution of the polychaete assemblages in the shelf and upper slope in this area in the NW Atlantic coast of Spain is described from samples collected during the 2002 and 2003 expeditions of the ‘DIVA-Artabria I’ project. Samples were taken at a transect composed of nine stations, covering a depth range of 150-1140 m. Three different sampling gears were used depending on the type of substrate: Epibenthic sledge, Agassiz trawl and Naturalist dredge. A total of 14,122 specimens belonging to 47 polychaete families were collected. Multivariate analyses identified two different groups of samples corresponding, respectively, to the continental shelf (150-400 m depth; soft bottoms) and upper slope (600-1000 m; stony substrata). Polychaete fauna from the shelf was composed of infaunal taxa such as ampharetids, opheliids, paraonids and

spionids; the upper slope was characterised by mobile epibenthic taxa such as syllids, hesionids, and phyllodocids.

Epibenthic polychaetes of the Bellingshausen Sea (Antarctica) collected by the Spanish Bentart project

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The Bellingshausen Sea (Antarctica) constitutes a natural connection between the Ross Sea and the Antarctic Peninsula and has zoogeographical importance because of its role in the dispersion of species around the waters of the Antarctic continent and with the South America through the Scotia Arc. Due to its remoteness and the prevalence of ice during most of the year, the benthic faunas of the Bellingshausen Sea have been less studied than those of the Weddell and Ross Seas and the Antarctic Peninsula. In consequence, little information is available on the polychaete fauna inhabiting the deep-sea soft bottoms at those areas. During the Antarctic summers of 2002-03 and 2005-2006, two expeditions under the auspices of the Spanish BENTART project were conducted on board the R/V Hespérides in the Bellingshausen Sea and the southwest coast of the Antarctic Peninsula. Benthic samples were collected at depths of up to 2043 m with two sampling devices: an Agassiz trawl for the epifauna and a Box-corer for the infauna. In this communication, preliminary results on diversity and distribution of assemblages of epibenthic polychaetes collected by means of the Agassiz trawl are presented.

Cosmopolitans and widely distributed species of black corals: case study for the North-East Atlantic

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Until quite recently black corals (Antipatharia: Anthozoa) were only sporadically reported from higher latitudes of the North Atlantic. However, after introducing methods of observations using remotely operated vehicles and manned submersibles it became obvious that black corals are important and rich components of suspension feeding fauna of the North-East Atlantic continental margin including banks and carbonate mounds (Weinberg et al., 2008; Roberts et al., 2008) as well as seamounts (Grasshoff, 1985, Molodtsova, 2005). Fauna of black corals of the North-East Atlantic was recently revised (Molodtsova, 2006) and was estimated to include 33 species. Of this number of species 18% and 21% were reported as having cosmopolitan or transatlantic distribution, respectively. In the present study we are

accented to several deep-sea species usually reported as having cosmopolitan or wide distribution, namely *Parantipathes larix*, *Bathypathes patula*, *Leiopathes glaberrima* and *Abyssopathes lyra*. Re-examination of specimens from published records showed that many records for mentioned species published in the literature are not reliable. Three species (*Parantipathes larix*, *Bathypathes patula*, *Leiopathes glaberrima*) reported previously as having wide or cosmopolitan distribution in fact appeared to include several species. It follows from these results that most of historical data on black corals cannot be recommended as it is for biogeographical constructions. *Schizopathes affinis* Brook, 1889 has to be considered as the only true cosmopolitan antipatharian in the North-East Atlantic. This work is a contribution to CenSeam, a project of the Census of Marine Life, and was supported by COMARGE, a project of the Census of Marine Life, and the RFBI Research Grant 09-05-00868.

New data on deep-sea sphaerodorids (Polychaeta, Sphaerodoridae) from Iceland and NW Spain (BIOICE and Diva-Artabria projects)

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Sphaerodorids (Polychaeta: Sphaerodoridae) are small polychaetes characterized by having the dorsum covered by a number of tubercles and papillae and are known to show a high diversity in the deep sea. Nevertheless, knowledge on sphaerodorids from many areas is still scarce, including those around Iceland and the northwest of the Iberian Peninsula. Those areas have, however, a great biogeographical importance because constitute the transition between Arctic and North Atlantic benthic faunas (Iceland) and between Boreal and Lusitanian areas (NW Iberian Peninsula). In this context, the BIOICE and DIVA-Artabria projects were devoted, respectively, to the study and characterization of the benthic faunas around Iceland and the Galician Continental Margin (NW Iberian Peninsula), including deep-sea areas of up to 2000 m depth. In this communication, taxonomic and ecological data on deep-sea sphaerodorid polychaetes collected during the aforementioned projects are presented. Some of the specimens found might represent new species to science.

Polychaete species diversity on the deep West Antarctic Peninsula shelf

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Polychaete species diversity is assessed on the deep West Antarctic Peninsula (WAP) shelf from a suite of samples taken in 500-600 m water depth on a transect close to Anvers Island,

Antarctica. 15 megacore samples were analysed to species-level from 3 sites, revealing 78 species of polychaete of which the majority may be new to science. Quantitative samples allowed an assessment of species abundances and the relative contribution of dominance to the overall species diversity. The composition of the assemblages varied across the shelf region, with the two outermost sites on the transect being relatively similar to each other but very different to the innermost station, which had higher diversity and a quite different species composition, possibly linked to changes in the sediment characteristics and degree of food availability. Species diversity, measured by rarefaction, evenness and species richness estimators was similar to values reported at other bathyal settings, but lower than that reported at temperate and tropical abyssal sites.

In situ hybridization with HRP end-labelled oligonucleotide 18S rRNA targeting probes for the identification of larvae and juveniles from chemosynthetic ecosystems

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More than thirty years ago, the discovery of deep-sea hydrothermal vents was an incredible breakthrough for the scientific community where everyone used to think that light was absolutely necessary for primary production. Indeed, these oases of life rest on their proper way for production of organic matter which is the chemosynthesis. Until now, four types of chemosynthetic ecosystems have been described: hydrothermal vents, cold seeps, whale and wood falls. These are really fragmented and isolated habitats that can be separated by tens to thousands of kilometres. However, same metazoan families or even species can be found at geographically distant, remote sites. This implies that these marine organisms must have developed high larval dispersal rates. As a consequence, identifying young stages turns out to be essential in order to evaluate these dispersal capabilities and better understand the connectivity between different habitats. Unfortunately, the morphological identification of marine invertebrate larvae down to the species level is often limited. Besides, collecting larvae is not straightforward. Special dedicated devices (CHEMOSYNTHETIC COLONIZATION OF LARVAL INVERTEBRATES devices (CHEMECOLIs) have been developed and deployed at hydrothermal vents (MAR) and cold seeps (Mud volcanoes and deep-sea fans) in eastern Mediterranean, Norwegian Sea and Atlantic Ocean. In order to identify recovered early stages, we developed a molecular method based on in situ hybridization of oligonucleotide probes with 18S rRNA. Specific oligonucleotidic probes were designed for the bivalve sub-family Bathymodiolinae and the polychaete family Spionidae, the two most common organisms found in CHEMECOLIs. Probes were labelled with the HorseRadish Peroxydase (HRP) enzyme allowing a colorimetric reaction-based detection of positives. We developed a protocol for testing probe specificity that can be applied to other probes. Probes were tested on pieces of adult tissue and on juveniles from several seep, vent and coastal species.

The distribution and species diversity of deep-sea foraminifera from the equatorial Pacific

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Deep-sea foraminifera are well known from studies by geologists that have documented the distribution and diversity of species living on the ocean floor (Murray, 1991, 2006). Most of our knowledge of these faunas concerns the hard-shelled, predominantly calcareous species, which are well represented in the deep-sea fossil record. However, deep-sea sediments abound in a variety of other foraminifera and foraminifera-like protists with agglutinated, often soft-shelled tests that are much more delicate than the calcareous species and have little fossilization potential. Many of these belong to poorly-known, single-chambered (monothalamous) taxa. Recent studies based on very fine sediment residues (32 microns) have revealed diverse assemblages of these morphologically simple monothalamous 'soft-shelled' foraminifera in the Pacific (Todo et al., 2005, Gooday et al., 2004 and Nozawa et al., 2006). We are currently analyzing similar assemblages at the Kaplan Central site (~130°W, ~14°N; ~5000 m water depth). Replicate sediment samples were obtained using a multiple corer from 3 stations in this area, which is located just below the carbonate compensation depth. At each site, 2 (Stn 866, 867) or 1 (Stn 873) complete cores (diameter = 95 mm) were subsampled using 3 cut-off syringes of 6.6 cm³ cross-sectional area. The 0-1 cm sediment layers (32 micron fraction) of these 15 subsamples together yielded 5618 individuals of rose-Bengal-stained benthic foraminifera, most of them (90%) soft-shelled morphologically types. A total of 199 species was recognised amongst this extensive collection. Some species, in particular the newly described *Saccamina minimus*, had an extremely patchy small-scale distribution on a scale of centimeters. For example, it was represented by 3, 1090 and 285 specimens in these subcores from one core. The reason for this patchy distribution is not clear but their density showed small-scale heterogeneity on the sea floor.

How an internet accessible database is helping us protect historical deep sea samples from the Challenger Expedition of 1872-76

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The Natural History Museum of London holds 28 million zoological specimens from around the world in its National Collection. Over 52,000 of these are from our oceans, many are historical and valuable "type" specimens such as those from the Challenger Expedition. Our online database (Ke Emu) enables researchers to access information on our national collection 24 hours a day 365 days a year. There are several search options including by expedition, ocean, species etc., also we have recently started populating our database with high quality images. The collection of image data serves several purposes, firstly this prompts a condition

survey of our most valuable, vulnerable material; secondly we take high quality raw data images providing a permanent record of the specimen should it be lost or damaged; and thirdly it allows researchers to access specimen images prior to arranging for example, a visit or specimen loan. This project will serve as a trial for the image data-basing and alternative access of a type collection. At present our first phase involves our 2,170 polychaete “type” specimens of which about a quarter are Challenger materials. We have completed 20% of the image data with 10% being added every 3 months.

Biogeography of the pan-distributed deep-sea coral genus *Chrysogorgia*

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Chrysogorgia is currently described as a pan-distributed octocoral occurring between 100-3375 m depth, but mostly >200 m. It is also regarded as one of the most speciose alcyonacean (soft corals and gorgonians) genera, with 63 currently-described species. While these characteristics could make *Chrysogorgia* a noteworthy model system for the study of radiation in the deep sea, genetic information on the genus is scant, and the monophyly of the genus has, to date, not been reported in the literature. We inferred a phylogeny of the genus from 296 specimens using the msh1 mitochondrial marker (700 bp), and used a subset of this collection to build a more resolved phylogeny based on 18S, msh1 and cox1 (2870 bp). We investigated biogeographic patterns using a database of sampling locations based on our collections, museum records, and a literature review. Forty-four msh1 haplotypes were characterized, one of which was found in both the Atlantic and the Pacific. These haplotypes formed a monophyletic clade. Most were rare, as 82% were represented by fewer than 10 specimens. Bathymetric, latitudinal and longitudinal ranges from the literature and museum collections completely overlapped ranges of specimens for which we obtained msh1 sequences, further establishing *Chrysogorgia* as a pan-distributed taxon. There was no latitudinal or longitudinal trend in the bathymetric distribution of *Chrysogorgia*, contrary to the expectation that emergence of deep-sea taxa would occur at high latitudes, where temperature variations between deep and shallow water masses are minimal. The rarity of most *Chrysogorgia* haplotypes prevented us from addressing their distributional patterns. In fact, even the spatial distribution of our best-sampled haplotypes (n>45) suggest that differentiating endemism from sampling artifacts is still a very challenging task.

Evidence of resource partitioning in deep-sea invertebrates based on stable isotope and pigment analyses

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Temporal changes in $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ isotopic composition and in phytoplankton pigments occurring in guts of deep-sea macro- and small megafauna invertebrates (infauna, epifauna, suprabenthos, and zooplankton) were studied within BIOMARE project. A wide range of physical-chemical factors were simultaneously analysed in the sampling, based on seasonal cruises performed in 2007 at bathyal depths (at 650-1100 m depth) off Catalan coasts, NW Mediterranean. Both stable isotopes and pigments analyses identified distinct trophic groups, from active suspension feeders to predators. These results were strongly consistent with previous information on diets of species, and suggest development of different feeding strategies in the bathyal benthopelagic system probably related to resource partitioning for food competition avoidance. Nevertheless, phytoplankton pigments of detritivore species overlapped with all other feeding modes most probably due to the consumption of different kinds of sinking particles (e.g. marine snow, phytodetritus), sedimented and frequently recycled POM, together with macrophyte remains. A secondary temporal tendency in food use was also observed, mainly depending on the condition of stratification or homogeneity of the water column, thus the seasonal trends must probably be related to changes in food availability and in trophic relationships. The seasonal pattern was more evident in species with feeding strategies more dependent on fresh organic matter (OM) inputs, such as detritivores and filter feeders. In these feeding groups, differential use of OM inputs was defined by seasonal variations in phytoplankton pigments present in the guts. In accordance with these results, environmental variables found to have a significant influence in feeding trends were strongly related to food inputs at bathyal depths. As an example, pigment content in guts was dependant on surface primary production taking place two months before sampling. Also it was related to water turbidity, which was also linked to changes in food availability by resuspension of deposited POM.

Taxonomy and distribution of the genus *Terebellides* and family Opheliidae (Polychaeta) in Icelandic waters, collected by the BIOICE project

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The present study is based on material collected under the BIOICE programme, started in 1992 and whose main objective is to broaden the knowledge of the distribution and abundance of the marine benthic fauna off Icelandic waters. Here, preliminary results on the

taxonomy and distribution of the polychaete genus *Terebellides* and the family Opheliidae in Icelandic waters are presented. Four species of *Terebellides* were identified; two of them were previously reported in the area (*Terebellides stroemi* Sars, 1853 and *T. williamsae* Jirkov, 1989); one was reported for the first time after the original description (*T. atlantis* Williams, 1984) and one is new to science. The new species is mostly characterised by the presence of two thoracic chaetigers with geniculate setae instead of one. Eight species of Opheliidae were identified: *Ophelia limacina* (Rathke, 1843), *Trachytrypae jeffreysii* McIntosh, 1879, *Ophelina abbranchiata* Stöp-Bowitz, 1948, *O. acuminata* Örsted, 1843, *O. cf. arctica* (McIntosh, 1877), *O. cylindricaudata* (Hansen, 1878), *O. cf. helgolandica* Augener, 1912 and *Ophelina* sp. characterised by a long and narrow anal tube provided with one ventral cirrus in basal position and several triangular distal cirri. Data on ecology and distribution around Iceland are presented for each species.

On the taxonomy and distribution of the deep-sea species *Axiokebuita minuta* (Hartman, 1967) (Polychaeta; Scalibregmatidae)

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Hartman (1967) described the scalibregmatid polychaete *Kebuita minuta* from the South Orkney Islands and Antarctic Peninsula. Two decades later, Pocklington and Fournier (1987) create a new species in a new genus, *Axiokebuita millsii*, from slope depths off Eastern Canada and propose the inclusion of *K. minuta* in this new genus. As these authors assigned three further specimens previously identified as *K. minuta* by Hartman (1978) and Blake (1981) to the new species, it is therefore considered a taxon with a bipolar distribution. According to those authors, the two species are distinguished by the presence in *A. millsii* of a “globular postsetal notopodial lamella”, which is supposedly absent in *A. minuta*. In this communication, taxonomy, distribution and ecology of the species is summarized and a redescription and comparison of *A. minuta* is presented from newly collected material in the Bellingshausen Sea and west coast of the Antarctic Peninsula, by the Spanish project BENTART (2006 cruise). Two previously unnoticed structures both from Antarctic and Norwegian specimens, i.e. a ciliated neck organ and a prostomial depression were observed under SEM and are here reported. *Axiokebuita millsii* Pocklington and Fournier, 1987 and *A. minuta* (Hartman, 1967) should be considered as the same species and the former is proposed as junior synonym of the latter.

Fatty acid compositions of muscle, liver and skull oil in deep-sea redfish *Sebastes mentella* over the Reykjanes Ridge

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The fatty acid profiles of neutral and polar lipids were analysed in tissues of muscle, liver and skull oil of the deep-sea redfish *Sebastes mentella* caught over the Reykjanes Ridge. The fatty acid compositions of both the neutral and the polar lipid fractions were tissue specific. The high amounts of the phytoplankton-derived omega-3 fatty acids 20:5n3 (eicosapentaenoic acid, EPA) and 22:6n3 (docosahexaenoic acid, DHA), in the neutral fractions of the muscle tissues clearly distinguished the muscle lipids from liver lipids and skull oil. In the skull oil, the fatty acid profiles of the neutral lipids were characterized by extremely high amounts of the long-chained mono-unsaturated fatty acids, 22:1n1, 20:1n9 and 18:1n9, indicating selective enrichment of these fatty acids. Of the tissues studied here, the neutral fraction of the muscle best reflects diet, while the skull oil is believed to be unsuitable in trophic studies. Interestingly, in the muscle oil, there were high amounts of docosahexaenoic acid, 22:6n3 (23%). Docosahexaenoic acid is a unique fatty acid important in the cell membrane, and the levels found in *S. mentella* are similar to those found in other deep-living fish species.

Microscale distribution, diversity and functioning of deep-sea benthic community in Atlantic Ocean and Mediterranean Sea

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Deep-sea ecosystems have been assumed to be spatially homogeneous environments for a long time, and the findings of extremely high levels of biodiversity in deep-sea ecosystems challenged our overall understanding of the patterns of distribution, diversity and functioning of deep-sea benthic communities. Although, in the last years much information has been gained on the distribution and functional role of the deep-micro and meio-benthos at large spatial scale, no investigation on the variability of these components (including viruses) and their interactions at fine spatial scale (of centimetres) is available. However, this is very important to identify the appropriate sampling strategy and for a better comprehension of the benthic food-webs and the entire deep-sea ecosystem functions. In the present study we investigated the spatial variability at the micro-scale level of the microbial (prokaryotic and viral) and meiofaunal communities in terms of abundance, biomass and diversity (diversity of bacteria, meiofaunal higher taxa and nematode's species diversity). Moreover, to explore the deep-sea benthic ecosystem functioning, at the cm scale, we also analyzed phytopigment and protein concentrations and functional variables such as enzymatic activities, heterotrophic prokaryotic production and meiofaunal biomass. To do this we selected two sites at 3000 m

water depth (North Atlantic Ocean and Eastern Mediterranean Sea), where we collected sediment samples using box-corer NIOZ type. Each box-corer was sub-sampled using a frame with 24 squares (5 cm X 5 cm). For each square we sampled the top 1cm of the sediment to analyze all of the structural and functional variables. Results from this study will allow providing a complete picture of the micro-spatial variability of all benthic components from viruses to meiofauna and to explore their functional interactions.

Cold water coral research in Iceland

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This poster provides an overview of the studies carried out at the Marine Research Institute on cold water coral (CWC) habitats in Icelandic waters. The main goals of these studies is to map the distribution of CWC habitats, characterize its accompanying fauna, investigate the interactions between coral habitats and fish and evaluate the damage caused by bottom fishing gears. The identification and mapping of coral habitat is based on the analysis of high resolution bathymetry data, on the location of live coral bycatch in research surveys and commercial fisheries, and on interviews with fishermen. Potential CWC grounds have been ground-truthed with video footage and photographs using a Remote Operated Vehicle (ROV) during two surveys. These surveys revealed live coral in the Reynisdjúp, Skaftárdjúp, Skeidarárdjúp, Hornafjardardjúp and Lónsdjúp areas. A portion of the Lónsdjúp trough (63.88°N, 14.03°W) has been selected as a case study area. Differences were found in species composition and abundance of fish and invertebrates (based on analysis of photographs and video material obtained with ROV) between CWC habitats and adjacent sites lacking coral. Evidence of damage to coral habitats includes fishing gears remains, turned and broken coral heads, plow marks and extensive coral rubble in locations at heavily trawled sites. High resolution fishing effort maps based on electronic logbooks are being used to evaluate the potential threat to coral habitats.

Litter accumulation at bathyal and abyssal depths in the Mediterranean Sea

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Marine litter has been defined by UNEP as “any persistent, manufactured or processed solid material discarded, disposed of or abandoned in the marine and coastal environment” (UNEP-Marine Litter a Global Challenge, 2009). The major sources of marine litter include coastal-originated waste, litter and pollution from ships, illegal dumping, lost or abandoned fishing gear and natural disasters. There is increasing evidence for the accumulation of litter in deep-sea habitats, but little is known on the impact on the fauna. Some potential impacts include suffocation, ghost fishing and the accumulation of persistent organic pollutants. Although

global conventions and agreements exist, marine litter is not usually dealt within policies or laws as a separate category of waste. Therefore, there is an urgent need to quantify litter accumulation in deep-sea habitats, to understand the impact on the ecosystem and develop management options. For the first time, litter accumulation at bathyal and abyssal depths has been described and quantified in the Mediterranean Sea in the framework of the PROMETEO (Blanes margin, NW Mediterranean) and BIOFUN (Western, Central and Eastern Mediterranean) scientific projects. The most abundant litter types are plastic, metal and glass, as well as discarded or lost fishing gear, and painting or oil wasting materials. The Blanes margin was sampled between 900 and 1500 m depth with an OTMS trawl in 2008-2009 and all collected litter was categorised and weighed. Litter accumulation was highest at the deepest station (1500 m) probably caused by a downslope accumulation effect. In 2009, the BIOFUN project sampled the western, central and eastern Mediterranean at 1200, 2000 and 3000 m depth. Litter was collected in all trawls at all sites and all depths. Although litter accumulation is slightly higher in the Western Mediterranean, no significant patterns with depth or longitude were observed. Our results highlight that litter is an important threat of deep-sea Mediterranean ecosystems. Further sampling and future dedicated projects are necessary to assess the impact of litter on the habitat and fauna.

Calcareous sponges from bathyal and abyssal depths of the Weddell Sea -- first record of deep-sea *Calcarea* in the Antarctic Ocean

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Calcareous sponges have traditionally been regarded as shallow water organisms, a persistent myth created by Hentschel (1923-25), partly supported by the problematic question of calcareous skeletal secretion under high partial CO₂-pressure below the CCD in the abyss. Up to now, only few species of the sponge class *Calcarea* have been described from depths below 2000 m world-wide. From the Antarctic Ocean, by far the largest number of records of *Calcarea* is known from shelf areas between 50 and 400 m depth. They have only been sporadically recorded on the lower shelf and the upper slope at depths between 570 and 850 m. From depths below 1000 m in the Antarctic there are no previous records of calcareous sponges. It was therefore a big surprise when the first true deep-sea *Calcarea* from the Antarctic Ocean were collected at depths between 1120 m and 4400 m during the ANDEEP I, II and III expeditions (Janussen et al. 2003a, 2006). All together, 5 calcarean species were collected from 5 different stations. 3 of these species were new to science and 4 have never been recorded in the Antarctic before (Rapp et al., in press). The 5 *Calcarea* species belong to 5 different genera and 5 families; they make up c. 7% of the total 76 sponge species, but only 1.6% of the about 500 sponge specimens collected in total during ANDEEP I-III. Taken the very patchy and isolated collections in the deep Weddell Sea, any generalization concerning the distribution of Antarctic deep-sea *Calcarea* should be done with caution. However, although calcareous sponges are rare in the Antarctic deep sea they seem to constitute a

constant component of the fauna. Therefore we assume that high proportion of calcarean sponge species new to science is still to be expected from the Antarctic deep-se

Macrofauna of shallow and deep hydrothermal vent fields on the mid-ocean ridges north of Iceland

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Deep-sea hydrothermal vents are usually associated with a highly specialized fauna, and since their discovery in 1977 more than 400 species of animals have been described. Specialized vent fauna includes various animal phyla, but the most conspicuous and well known are annelids, mollusks and crustaceans. The newly discovered deep sea hydrothermal vents on the Mohn and Knipovich ridges north of Iceland hold a unique biodiversity. The shallow field consists of two main areas with low temperature white smokers and brine seepage, located at 5-700 m, while the deeper Loki Castle vent field at 2400 m depth consists of a large area with high temperature black smokers. We have investigated the fauna collected around these new sites. The shallow hydrothermal vent sites show low abundance of specialized hydrothermal vent fauna. Single groups (i.e. Porifera and Mollusca) have a few specialized representatives but groups otherwise common in hydrothermal vent areas are absent. Up until now slightly more than 200 macrofaunal species have been identified from this vent area. The fauna is, with few exceptions, an assortment of bathyal species known in the area. The deeper area contains a much more diverse vent endemic fauna with high abundances of specialized polychaetes, gastropods and amphipods. Our data indicate that the fauna composition is a result of high degree of local specialization in combination with a migration of vent fauna into the Arctic Ocean from the Pacific Ocean rather than from the Atlantic Ocean.

Presence of *Osedax* on seal bones in the Monterey Submarine Canyon

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Hydrocarbon degradation by *Osedax* worms likely plays a large role in the carbon cycling of large deep-sea food falls. To assess preference of *Osedax* on non-whale based sources, seal carcasses were placed at two locations in the Monterey Submarine Canyon. The first carcass (seal A), an adult elephant seal, was anchored to a 3' X 8' open lattice frame and placed 50 m adjacent to an existing whale fall at 630 m. Since *Osedax* were shown in to be non-whale-fall specialists, colonizing on cow bones placed near existing whale fall sites, seal B was deployed directly on the sediment at an 880 m site where no known whale carcass existed within several kilometers. Mitochondrial cytochrome C oxidase subunit I sequences were used to identify *Osedax* species found on bones from seal A and seal B. Within 10 weeks of

deployment, *Osedax* colonized seal bones collected from these sites. A cabled intensified camera system recorded tissue removal by macrofauna from seal B for 4 months after deployment of the carcass. In this talk, we will present an overview of *Osedax* species found on seal bones at two depths. We conclude that *Osedax* colonize a variety of bone sources at and away from existing whale-fall sites.

A re-description of the deep-sea protobranch bivalve *Ledella ultima* (E. Smith, 1885) with notes on reproduction and ecology

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During a recent expedition to the abyssal South Atlantic (Cape and Agulhas Basins), two morphotypes of the small protobranch bivalve *Ledella ultima* (E. Smith, 1885) (<3.5 mm) were collected by RV Polarstern at depths below 4500 m, using an epibenthic sledge and Agassiz trawl. Here, we present data on all individuals collected exhibiting typical growth with concentric growth rings and a number of specimens also showing vertical growth perpendicular to the concentric shell margin (secondary growth). Those with secondary growth exhibit a more convex dorsal margin and stronger yellow colouration around the secondary growth bands. Size ratios and growth ring counts are presented for the two morphotypes. Scanning electron microscopy revealed a large prodissoconch I with prodissoconch II appearing to be absent from both morphotypes suggesting non-feeding larval development. Internal layout is dominated by a large coiled gut formation containing soft sediment and reduced ctenidia indicating deposit feeding and distinct gonads. Dimensions of the individuals demonstrating secondary growth are significantly different to those without, but the ratio of height:length and breadth:age does not significantly change. This suggests that concentric growth around the umbones occurs at a constant rate before secondary growth increases bivalve breadth and internal volume with age. Notes on the ecology and reproduction are discussed with further evidence from histology.

Benthic trophodynamics on the Mid-Atlantic Ridge: a stable isotope approach

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The Mid-Atlantic Ridge (MAR) is a large topographically complex habitat with a mixture of hard rock and sediment filled terraces. Previous trophic studies have focused on localised areas of chemosynthetic activity and to a lesser extent the pelagic realm, leaving benthic areas, dependent on the downward vertical flux of organic matter, relatively unexplored. Trophic relationships of benthic macro-consumers on the MAR, under areas of hypothesised

varying seasonal surface productivity north and south of the Charlie Gibbs Fracture Zone (CGFZ) were investigated using stable isotopes of carbon, nitrogen and sulphur. Examination of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ suggest differences in energy flow and trophic relationships between the two stations. Benthic-pelagic and benthic fauna appear to separate into two different food chains in accordance with their stable isotope values. The range of $\delta^{13}\text{C}$ at the north and south stations were close suggesting similar energy sources but two energy sources are hypothesised to be present; 1) a pelagic source (-20‰ to -18‰) entering the benthic system through vertically linked food chains, and 2) a sediment source (-18‰ to -16‰) originating from the downward flux of phytodetritus. A tighter coupling between the deposit feeding invertebrates and the sediment energy source was apparent at the southern station. This may indicate a greater reworking of the sediment in relation to the way food is supplied to the benthic system. However, north of the CGFZ the pelagic energy pathway appears clearer. In some cases $\delta^{15}\text{N}$ of deep-sea fish and benthic invertebrates were comparable which would suggest they shared a similar trophic position. However, their difference in $\delta^{13}\text{C}$ would suggest these fauna are utilising different energy sources. Overall, the results suggest mobile predators can by-pass the benthic food chain while the pathways by which energy enters the system may be influencing the trophodynamics at the northern and southern stations.

Preliminary results on molecular phylogeny for genus *Deania* (Elasmobranchii: Centrophoridae) from the NE Atlantic with implications on the taxonomy of the group

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The genus *Deania* is represented by four species, 3 of which are inhabiting the NE Atlantic. The morphology leaves no doubts in discriminating *D. profundorum* from the others due to the presence of a subcaudal keel underneath the caudal peduncle, as well as *D. quadrispinosum* for its extremely long snout, short and high first dorsal fin. Much more similar are the other two species, *D. calcea* and *D. hystricosa*, which are in turn identified by the roughness of their skin. Geographical distribution is somehow different as *D. calcea* extends to higher latitudes, *D. quadrispinosum* is not encountered above the equator, while *D. hystricosa* is recorded in the N Atlantic up to the latitudes of Madeira and Azores, where they live in sympatry with *D. calcea*. In this study we are characterising the phylogeny of the genus *Deania* using mtDNA markers, Cytochrome Oxidase subunit I and Control Region, to elucidate the taxonomical status of each of the species inhabiting the NE Atlantic.

Morphology and DNA to complement each other in deep-sea isopod taxonomy

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Taxonomic problems in species delimitation and cryptic species have been reported from a range of asellote isopod taxa. Thus, biodiversity of deep-sea Isopoda may be largely underestimated. Species delimitation is essential, though, as species are routinely used as fundamental units in e.g. biogeographic studies. Morphology and molecular data provide two distinct character systems to complement each other. Consequently, the integration of classical taxonomy and DNA barcoding has been urged as a joint effort to describe biodiversity. With its multiple taxonomic questions, the deep-sea isopod family Macrostylidae (Hansen, 1916) seems to be an excellent model taxon to test the applicability of molecular techniques in deep-sea isopod taxonomy. For this study sequence divergences have been evaluated from three mitochondrial and three nuclear loci for their appropriateness in species delimitation. This provides a first step to make DNA barcoding a standardized method in deep-sea isopod research and may then assist linking morphologically disparate life history stages and facilitate the identification of damaged specimens or dimorphic sexes in the future.

Wood-boring bivalves from a NW Mediterranean deep sea canyon: abundance and biomass of *Xylophaga* spp. (Mollusca, Bivalvia)

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The Prometeo, a multidisciplinary project focusing on the Blanes submarine canyon (NW Mediterranean), allowed us to investigate the organisms associated with marine wood falls inside the canyon and in the adjacent open slope. Three replicate experimental traps with pine and oak were deployed at different depths (900, 1200, 1500, 1800 m) and collected after 3, 9 and 12 months.

Samples were colonized by three new species of *Xylophaga* (deep-sea wood-boring bivalves) which differ from the previously known species and, thus, are here reported as *X. near dorsalis*, *X. near heterosiphon* and the rare species *X. near clenchi*.

We measured the shell height, length and width of all intact specimens, as well as the incurrent and excurrent siphon lengths. Wet, dry and ash free dry weights were measured in selected specimens to estimate their relationships with shell length, which were then used to estimate the total biomasses.

The abundances of both *Xylophaga* species inside the canyon were significantly higher than in the adjacent slope. *X. near dorsalis* was the dominant species and its abundances were higher at 900 and 1200 m deep, while *X. near heterosiphon* preferentially colonized pine.

Our study confirms the role of Blanes canyon in trapping sediments and organic matter of terrestrial origin, which strongly influence and favours the development of specifically associated fauna. Moreover, the presence of a large larval pool of *Xilophaga spp.* waiting for recruitment opportunities inside the deep canyon clearly reflects the high influence and the frequent presence of these terrigenous inputs, likely linked to the outflow of the Tordera river.

Biodiversity and distribution of the genus *Gromia* (Protista, Rhizaria) in the deep Weddell Sea (Southern Ocean)

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We provide a survey of morphospecies of *Gromia*, a genus of testate protists, from bathyal and abyssal depths in the Weddell Sea and adjacent areas of the Southern Ocean. This material represents the most extensive and diverse collection of deep-sea gromiids so far recorded. The twelve species, nine of which are undescribed, are recognized on the basis of morphological criteria, including the test size and shape, the appearance and structure of the oral capsule, and the characteristics of the test wall. Most species have a single oral capsule, which is circular in plan view with a conical nipple-like shape in lateral view. One morphospecies has three oral capsules. The appearance and structure of the wall displays great variability between *Gromia* species, ranging from very delicate and transparent with highly reflective highlights to relatively thick with distinct patterns of ridges covering the surface. More often, however, differences in wall structure are more subtle. Most morphospecies were distributed at bathyal depths along the continental margin, but one was sampled at ~ 4800 m, representing the first record of an abyssal gromiid. Concurrent with findings from other regions of the World's oceans, the Weddell Sea gromiids were mostly found in surficial sediments in areas of elevated organic input, suggesting that deep-sea gromiids are likely to play an important role in carbon cycling in bathyal eutrophic regions through the ingestion and degradation of fresh organic matter.

Deep-ocean observatories in Europe

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The needs for a network of ocean observing systems cross many areas of earth and marine science. Understanding from existing studies is fragmented to the extent that it lacks the coherent long-term monitoring needed to address questions at the scales essential to understanding climate change and improve geo-hazard early warning. Data sets from the deep sea are particularly rare with long-term data available from only a few locations, the longest

of which extends back about three decades. These science areas nonetheless have direct impacts on societal well being. There is now wide recognition that research addressing science questions of international priority, such as understanding of the potential impacts of climate change or geo-hazards like earthquakes and tsunamis should be conducted in a framework that can address questions across adequate temporal and spatial scales. The European Seas Observatory NETWORK Network of Excellence (ESONET NoE) and EuroSITES programmes aim to increase our understanding of the deep-sea and its coupling to the surface ocean and climate change, as well as marine geo-hazards. Substantial efforts are now underway to realise an urgently needed network of deep-sea observatories around European Seas including the European large-scale research Infrastructure programme EMSO (European Multidisciplinary Seafloor Observatory). The development of ocean observatories provides a substantial opportunity for ocean science to evolve in Europe. This network will provide the means to collect standardized data capable of bridging various measurement scales across a dispersed network in European Seas adding greatly needed certainty to estimates of future oceanic conditions. The connection of ocean observatory research into larger frameworks including the Global Earth Observation System of Systems (GEOSS) and the Global Monitoring of Environment and Security (GMES) programme is integral to its success. It is in a greater integrated framework that the full potential of the component systems will be realised.

Comparative analysis of feeding and diet in bathyal sea anemones and gastropods: evidence of dietary feedback in a mutualistic association

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The diets of epibiotic sea anemones *Allantactis parasitica* and their gastropod hosts were analyzed using digestive tract contents, lipid biomarkers and observations of live specimens in an attempt to detect differences between symbiotic and asymbiotic individuals. A total of 78 gastropods carrying 126 *A. parasitica* were collected at depths of 191-627 m in the northwest Atlantic. Asymbiotic individuals, i.e. 18 *A. parasitica* living on inert substrata and 10 gastropods devoid of epibionts, were also sampled. Gastropods carrying one or two epibionts had higher stomach indices than those harbouring three epibionts or no epibiont. The diet of symbiotic gastropods was also more diversified based on stomach contents and lipid analysis. Gastrovascular content indices of asymbiotic sea anemones were generally lower than those of symbiotic counterparts. Their gastrovascular cavities were more often empty, and their diet less diversified with fewer benthic items, suggesting that foraging of gastropods through the sediments makes more food available to sea anemones living as epibionts. Lipid analysis showed some disparities between symbiotic and asymbiotic sea anemones at the regional scale, including in percent phospholipids and in the proportion of certain fatty acids. Together these findings indicate that mutual protection against predators may lead to prolonged and more efficient foraging for gastropods and increased time spend deployed (feeding) in food-rich areas for sea anemones, thus enabling a fuller exploitation of limited food resources available at bathyal depths.

The role of eruptions and disturbances on the resilience and connectivity of mid-ocean ridge and seamount chemosynthetic communities

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The resilience of deep-sea chemosynthetic communities to disturbance largely depends on the degree of connectivity among these disjunct populations. Understanding the processes of in mid-ocean ridge and seamount environments requires knowledge of the temporal and spatial scales over which those processes occur. Over the past 17 years, the detection and now “direct observation” of more than nine seafloor eruptions and even more numerous and diverse geologic disturbances (e.g., dyking and cracking events) have provided a broad spectrum of perturbing seafloor phenomena that serve as key agents for creating new vent habitat, providing bursts of nutrients, supporting blooms of microbial and macrobiological communities, imparting magmatic/hydrothermal fluxes, controlling fluid geochemical composition, altering the successional stage of faunal communities, guiding the temporal and spatial scales of local extinction and recolonization, and for directing the evolution of physiological adaptations. Eruptions have now been documented on the East Pacific Rise, Southern Mid-Atlantic Ridge, Gakkel Ridge, Galapagos Rift, CoAxial, Northwest Rota, West Mata, and Loihi Seamounts, representing diverse emergent eruptive styles, from explosive pyroclastic deposits to thin lava flows, these processes are occurring in different biogeographic regions hosting different regional species pools. Recent results of manipulative temporal experiments, designed to examine the simultaneous role of fluid chemistry and microbial biofilms on the larval settlement and distribution of fauna, and metapopulation genetic and connectivity studies of post-eruptive colonizers will be discussed to provide a contextual framework with which to interpret the affect eruptions and disturbance have on ecological interactions in different biogeographic regions of the world, and the timescales over which they vary.

Tube extension and reproduction of *Lamellibrachia satsuma* inhabiting a whale vertebra under laboratory condition

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Vestimentiferan tubeworms (Annelida: Polychaeta: Siboglinidae) inhabit sulfide-rich environments, and harbor sulfur-oxidizing bacteria as symbionts intracellularly for nutrition. The vestimentiferan tubeworm *Lamellibrachia satsuma* is a dominant species at seeps in Kagoshima Bay. This species are also known to inhabit whale vertebrae that were

experimentally deployed beside its natural habitats. More than 300 individuals (named as WF *L. satsuma*) were kept well in an aquarium for more than one year at atmospheric pressure with one vertebra that was retrieved 3 years later from the deployment and released a certain amount of hydrogen sulfide. The tube extension of the WF *L. satsuma* at both anterior and posterior ends was measured by use of a tube-staining method. Tube-forming processes were observed using a time-lapse imaging system. Tube extension rate of posterior end was one order of magnitude faster than that of the anterior. Tube forming processes were different between anterior and posterior ends. The posterior ends grew continuously but the anterior showed resting phases. The total tube extension rate of the WF *L. satsuma* in this study was estimated as 42.6 cm yr⁻¹, which was much faster than that in previous study (0.7 cm yr⁻¹). The WF *L. satsuma* occasionally spawned, and more than 100 individuals were newly settled on the vertebra under aquarium condition. Many eggs and cleaving embryos were collected from the aquarium, which were identified as *L. satsuma* by using molecular techniques. Elongated male pronucleus was observed in most eggs. These results strongly indicated its successful reproduction under laboratory condition.

High-pressure tolerance in larvae of the ditch shrimp *Palaemonetes varians*

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The effect of pressure on shallow-water fauna is key to understanding the evolutionary adaptations observed in their deep-sea relatives. The ditch shrimp *Palaemonetes varians* has a monophyletic relationship with deep-sea hydrothermal vent shrimps of the family Alvinocarididae. Here, we investigate the temperature and pressure effects on survival, development and energetic contents of the first larval stage of the shallow-water shrimp *P. varians*. In this stage *P. varians* shows facultative lecithotrophy. Development is observed across a temperature tolerance window of between about 10 and 30°C, and at pressures up to the equivalent of at least 1000 m water depth. Larval developmental time is shown to scale with temperature. Tolerance to high-hydrostatic pressure is greater at 20°C. A slower development and an increase in mortality are observed with increasing pressure. The tolerance to high pressure found in the early ontogeny of *P. varians* may be a trace of an adaptation expressed by an ancestor that lived at greater depth, or with a wider depth range distribution. It is likely that any such ancestor would have exhibited similar adaptability to changes in temperature or pressure.

Temporal variability in polychaete assemblages of the abyssal NE Atlantic Ocean: the species response

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Temporal variability in species from three dominant deep-sea polychaete families, Cirratulidae, Spionidae and Paraonidae, was assessed over a 9-year period. Samples were studied from Porcupine Abyssal Plain, NE Atlantic Ocean from 8 cruises between August 1989 and September 1998. From September 1996 and March 1997 megafaunal and foraminiferal elements of the abyssal fauna dramatically increased in abundance. This increase was most marked in the holothurians and one species in particular, *Amperima rosea*. Coinciding with these increases in megafaunal abundance, species from two of the three most abundant families, Cirratulidae and Spionidae, also showed significant increases in numbers of individuals. Six species were identified as having increased abundance coinciding with the *Amperima* Event during July and October 97. However, not all species responded in the same way and at the same time. Indeed some species showed no response at all. The species level response among polychaetes was for the most part from those existing elements of the fauna and not new immigrants. This study illustrates the importance of assessing faunal responses to environmental change at the lowest taxonomic level possible.

Key questions of the IceAGE Project: selected crustacean taxa as example groups

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The area around Iceland is characterised by several local peculiarities like submarine ridges and influence of various water masses of different origin. The BIOICE project (Benthic Invertebrates Of ICElandic waters, 1991-2004) was designed to investigate the faunal composition as one of the most extensive studies (1500 stations, 3670 samples and > 3 mill. individuals) around Iceland on both sides of the Greenland-Iceland-Faeroe (GIF) Ridge in depths between 30 – 3000 m. In addition, abiotic parameters have been collected. The state of the art of BIOICE results with the main focus on selected Isopoda and Amphipoda (Crustacea) will be reviewed under the influence of the GIF Ridge as geographic barrier. Based on distribution data from recent publications, the key question of the new project IceAGE (Icelandic Marine Animals: Genetics and Ecology) will be presented. The IceAGE project aims at combining classical taxonomic methods with modern aspects of biodiversity research, in particular phylogeography (population genetics and DNA barcoding) and ecological modelling in the climatically sensitive region around Iceland. The talk gives a perspective, based on the examples that the sampling within IceAGE will provide the possibility to solve taxonomic problems with help of molecular methods.

Deep-sea fishes of the Mid-Atlantic Ridge: results of the 2009 Henry Bigelow Expedition

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As part of an ongoing study of the northern Mid-Atlantic Ridge biodiversity and ecology (CoML field project MAR-ECO), a detailed survey of the pelagic and demersal fishes in the region of the Charlie-Gibbs Fracture Zone (~ 600 n.m. south of Greenland) was conducted. A total of 17181 pelagic fishes (92 spp., 35 families) were sampled from 0-3000+ m, with the Myctophidae the most species-rich. The bristlemouth *Cyclothone microdon* was by far the dominant species in numbers (82% of total), while the sawtooth eel *Serrivomer beani* dominated biomass (27%). A total of 441 deep-demersal fishes (28 spp., 13 families) were sampled from 600-3000+ m, with the Macrouridae and Alepocephalidae comprising half of species numbers. The abyssal halosaur *Halosaurus macrochir* was most abundant, while the abyssal grenadier *Coryphaenoides armatus* contributed the most biomass. Remarkable among the pelagic fish data were routine shallow catches of bathypelagic fishes (see A.B. Cook et al., this volume), and among the demersal fishes were the large size of the individuals, above or near the maximum known for many species. The high species number relative to sample number portends the enhanced deep-sea biodiversity about abrupt topographic features, while the lack of asymptote of species number versus sampling effort underscores our incomplete inventory of this biodiversity.

Distribution and trophic ecology of *Bathylagus euryops* (Teleostei: Microstomatidae) along the northern Mid-Atlantic Ridge

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The assemblage structure and ecology of meso- and bathypelagic fishes are poorly known in general, particularly over mid-ocean ridges. In June 2004, the month-long MAR-ECO (Census of Marine Life) research expedition aboard the R/V G.O. Sars sampled the deep-pelagic fauna over the northern Mid-Atlantic Ridge with the objective of quantitatively assessing the nekton associated with the ridge from Iceland to the Azores. A total of 115 discrete-depth trawl samples were taken from the surface to depths of 3000+ meters using two different double-warp midwater trawls, one of commercial fishing size (a large 'Akra' trawl) and one of oceanographic research size ('Macroplankton' or 'Krill' trawl). Catch data revealed the deep-sea smelt *Bathylagus euryops* to be the biomass dominant species,

accounting for over 28% of total biomass, as well as being the 3rd most abundant species along the MAR. Further distributional analyses elucidated a trend in decreasing biomass from north to south with a biomass maximum around 1500-2000 meters. Understanding the food-web structure and organic cycling of deep-pelagic ecosystems is critical for increasing our knowledge of the distributional patterns of deep-sea fishes. Preliminary results indicate that gelatinous zooplankton represents a significant component of the diet of *B. euryops*. Molecular probes are currently being developed to identify these prey items in this, and other fishes that consume gelatinous zooplankton.

Preliminary data on the bathyal amphipods from the Golfo Ártabro (Galicia, NW Iberian Peninsula)

Tato R., García-Regueira X., Lucas Y., Moreira J. and Urgorri V.

Estación de Biología Mariña da Graña

The order Amphipoda is one of the most diverse and extended groups of marine crustaceans around the world, from littoral depths to abyssal plains. Two different expeditions were done in October 2002 and 2003 under the auspices of the DIVA ARTABRIA I project. This project was aimed to study the deep sea fauna in the West coast of Galicia (NW Spain). During these expeditions, three different gears were used to take the samples on the shelf and the upper slope of the Golfo Artabro (Agassiz Trawl, Naturalist dredge and Epibenthic sledge) in one transect covering a depth range of between 150 and 1140 m. In this communication, preliminary results on the composition and ecology of amphipod assemblages are presented. In total, 16 families were identified being lysianassids and oedicerotids the most important groups in abundance and number of species. Several different assemblages were observed according to depth and nature of substrata.

***Heteromesus* species occurring off South Iceland - morphology and distribution**

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The family Ischnomesidae (Crustacea: Isopoda: Asellota) is a pronounced deep sea family comprising little over 100 known species in the world oceans. Species in the family have an elongated body, subcylindrical and narrow and impregnated with calcium carbonate. The family is unique amongst the isopods in having the fifth pereonite (body segments) at least twice as long as wide and the head completely fused to the first pereonite. The family consists of seven genera (*sensu lato*) with most of the species in four genera. Three genera have been found in Icelandic waters, i.e. *Haplomesus*, *Heteromesus* and *Ischnomesus*. The genus *Heteromesus* comprises 16 described species found only in the northern part of the Atlantic Ocean and the Nordic Seas / Arctic Ocean, but only 3 species have been reported in Icelandic waters, i.e. *H. dentatus* Hansen, 1916, *H. frigidus* Hansen, 1916 and *H. schmidtii* Hansen,

1916. *H. frigidus* has been found at a number of locations north of the Greenland-Iceland-Faeroe Ridge (GIF - Ridge), while *H. dentatus* and *H. schmidtii* have only been reported earlier from single locations south of Iceland. During the BIOICE project, specimens of *Heteromesus* were sampled at 119 stations out of 581 sample stations, 61 stations north of the ridge and 58 stations south of the ridge. At least five species of *Heteromesus* were found in Icelandic waters. North of the ridge only *H. frigidus* was found, but south of the ridge four species were found, i.e. *H. dentatus*, *H. schmidtii* and also two *Heteromesus* species earlier not known in Icelandic waters, *Heteromesus longiremis* earlier found in Davis Straight and *Heteromesus* sp. C, presumably new to science. These four species are presented, the location of the sampling stations where they were found are shown and the difference in their morphology is discussed.

A new record of *Laevipilina rolani* (Mollusca, Monoplacophora) from the Galician Bank (NW Iberian Peninsula) collected in the expedition DIVA-Artabria II-2009

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In October 2009 the University of Santiago de Compostela led the oceanographic expedition DIVA-Artabria II-2009 on board the Spanish oceanographic research vessel R/V Sarmiento de Gamboa. The expedition aimed to prospect the deep benthos of the Galician Bank, a seamount located in the west of the Galician coast (NW Iberian Peninsula). 32 stations were sampled with different types of substratum (rock, stones, nodules, coral, gravel, sand and mud) in depths between 620 m on the peak to 5,307 m on the adjacent Iberian Abyssal Basin. Samplings were carried out with different types of dredges: rock dredge, epibenthic sledge, Agassiz trawl, box-corer and multicorer. In Station 21 located on the SSE slope of the peak, a transect line was set between the points 42° 28.5375' N; 11° 58.1547' W and 42° 29.1281' N; 11° 57.2647' W. The sampling of Station 21 was carried out with the rectangular rock dredge, in a bottom of carbonated crusts and stones covered in abundant epifauna between 1,434-1,348 m deep with a total dragging time of one hour. Among the sessile epifauna, a shell of a monoplacophoran mollusc of the genus *Laevipilina* appeared half-covered by a sponge. A later study in the laboratory proved it to be a specimen of *Laevipilina rolani* described by Waren & Bouchet (1990) from a station 25 miles further to the north of the Galicia Bank. The second record of this species was done by Urgorri & Troncoso (1994) from the continental slope of the west of Galicia. In this paper, a thorough study of the shell at SEM is presented, comparing it with the other specimens known from the species and with *L. cachuchensis* described by Urgorri, García-Álvarez & Luque (2005) from the continental slope of the North of the Iberian Peninsula.

Analysis of the flexibility and adaptation of *Halomonhystera disjuncta* using the latest molecular technology

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Nematodes are one of the most abundant and diverse metazoan phyla in terms of species richness and are found in a lot of different environments. This project is focusing on the flexibility and adaptation of the nematode *Halomonhystera disjuncta*. The nematode has been observed at different shallow water habitats and has been reported as a dominant species at the Håkon Mosby Mud Volcano (HMMV, SW Barents Sea slope, 1280 m). This mud volcano is characterized by the seepage of methane-containing waters together with fluidized (H₂S) muds through the seabed, generating a continuous energy (chemosynthetic) and carbon supply for the benthic community. The second environment of interest is the Paulina polder tidal flat, located in the lower part of the turbid, nutrient-rich and heterotrophic Westerschelde estuary. To elucidate the flexibility and adaptation strength of *H. disjuncta*, its transcriptome (from both environments) will be analyzed. In addition to this analysis, the lipid composition of the nematode in both environments and the survival rate and CO₂ production (metabolic rate) of *H. disjuncta* under different environmental parameters (temperature, sulfides, oxygen,...) will be analyzed in the hope to correlate these results to the previously obtained transcriptomic dataset.

Hydrothermal vent fauna on the Southern Mid-Atlantic Ridge and biogeographic association with other chemosynthetic habitats

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Do large fracture zones and deep water currents affect the dispersal of hydrothermal vent organisms and thereby determine vent biogeography along ridge axes? The equatorial Atlantic is an ideal area for investigating this question. It has been hypothesized that the massive Romanche and Chain fracture zones in combination with strong currents along and through these fracture zones act as physical barriers, preventing the dispersal of vent fauna along the Mid-Atlantic Ridge (MAR). We have investigated the distribution of fauna from the recently discovered hydrothermal vents along the southern Mid-Atlantic Ridge between 4 – 11°S and compared it with fauna from the known vents along the northern MAR. We focused on the bivalves *Bathymodiolus* spp. and *Abyssogena* sp., the vent shrimp *Rimicaris exoculata* and the symbiotic bacteria associated with these host groups. Our molecular analyses show that the equatorial fracture zones are not a major physical barrier between vents from northern and southern MAR vent sites.

The food web structures of three canyon regions revealed by linear inverse modeling and network analysis

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NIOO-KNAW
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We will present carbon-based food web models that were constructed for the upper (300 – 750 m water depth), middle (2700 – 3500 m) and lower region (4000 – 5000 m) of the Nazaré canyon (eastern Atlantic Ocean) using linear inverse modeling. The food web models were constructed based on a large empirical dataset consisting of biomass and carbon processing data, and general physiological data constraints from the literature. Large differences were found between the three regions. Total carbon input into the food webs of the upper and middle region was of similar magnitude (8.41 ± 0.66 and 12.0 ± 0.70 mmol C m⁻² d⁻¹ for the upper and middle region, respectively), though partitioned differently amongst the organisms. The upper region was bacterially-dominated, with the dominant fate of detritus being dissolution to DOC and subsequent respiration by bacteria (83% of total respiration). Canyon-specific conditions that result in high OM input in the middle region seem to be mostly beneficial for deposit-feeding holothurians (56% of total respiration), whereas bacteria accounted for 41% of the total respiration. This pattern of carbon processing as found in the middle region resembled that found in shallower continental shelves and upper slopes. Carbon input into the lower region was lower (2.48 ± 0.03 mmol C m⁻² d⁻¹), but the pattern of carbon cycling was more similar to the upper region, though even more strongly bacterially-dominated (95% of respiration), and resembled that of abyssal plain food webs. The contribution to total respiration by meiobenthic (13% in the upper and <5% in middle and lower region) and macrobenthic (<4%) was limited in all regions. The sedimentary food webs in the Nazaré canyon seem to have a distinct “meiobenthic food chain” that is only loosely connected to the higher trophic levels. The viral shunt, i.e., recycling of carbon between dissolved organic carbon and bacteria due to viral lysis, was quantitatively important in the upper and lower region and resulted in comparatively high levels of carbon recycling. The high biomass and contribution to carbon cycling of megabenthos in the middle region caused recycling of carbon within the food web to be suppressed as compared to the other regions. Network indices that relate to food web stability and maturity indicate that the food web in the lower region is less stable and mature, which is surprising since this food web seems to be less affected by the canyon than the other two regions.

Genetic population structure of the Portuguese dogfish *Centroscymnus coelolepis* within the Eastern Atlantic

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The Portuguese dogfish *Centroscymnus coelolepis* is a deepwater squaloid shark found over continental and insular slopes, and mid-ocean ridges in the Atlantic, Indian and western Pacific oceans. Its bathymetric distribution varies regionally but off western Europe the species is often caught in several trawl and longline fisheries operating between 500 and 1700 m. Although the Portuguese dogfish has recently been declared depleted in the eastern North Atlantic, there is still limited knowledge about the species' biology, ecology and population structure throughout its range. In this study, the pattern of population structure of the Portuguese dogfish along the eastern Atlantic was evaluated using eight polymorphic nuclear microsatellite markers and a 496-bp fragment of the mitochondrial DNA control region (mtDNA CR). Sample collections (20-50 individuals/location) were obtained from slope waters off Ireland, mainland Portugal, Madeira, Mauritania and South Africa, as well as from the mid-Atlantic ridge off the Azores. Overall, high levels of genetic diversity were found at the nuclear microsatellite loci although low diversity was found in the mtDNA CR. Levels of genetic diversity were similar among sample collections and no genetic differentiation was detected among collections with either nuclear or mitochondrial markers. Our results indicate that there is sufficient gene flow among fish sampled from locations separated by hundreds or thousands of miles to prevent the accumulation of marked genetic differences. The absence of genetic divergence not only among locations along the continental slopes of the eastern Atlantic but also between slope waters and the Azores, suggests that there are no major environmental barriers for individual dispersal throughout the study area. Also, since dispersal in the yolk-sac viviparous Portuguese dogfish implies active swimming rather than passive drift, our results suggest that the species is capable of long distance movements.

Enhanced megafaunal abundance and diversity in submarine canyons on the Oceanic Islands of Hawaii

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Submarine canyons are important sources of habitat heterogeneity on the slopes of continents and islands, but canyon studies have been largely restricted to continental margins. We use visual and video surveys from 36 submersible dives to evaluate canyons as abundance and diversity hotspots for megafauna in the Hawaiian Archipelago, an island chain embedded in an oligotrophic ocean. We surveyed megafauna in canyon and slope settings at depths of 350 – 1500 m along the margins of four islands: the low “islands” of Nihoa and Maro Reef, and the high islands of Oahu and Moloka'i. Megafaunal communities in canyons differed significantly from those in nearby slope habitats at all depths. Highly mobile fishes and

invertebrates were more abundant in canyons than on nearby slopes on all islands suggesting that canyons may be important sources of larvae for surrounding habitats. Where total megafaunal abundances were similar or higher on the slope, the differences were driven by sessile animals likely to have difficulty with high currents and sediment transport in canyons. Megafaunal species richness and diversity trended higher within canyons, especially for the highly mobile taxa. Canyons contained 41 megafaunal species never observed on the slope, and increased estimated regional species richness by 25-30 species, indicating that canyons enhanced beta and gamma (regional) biodiversity. We conclude that submarine canyons on both low and high islands in the Hawaiian Archipelago, and on oceanic islands in general, may provide keystone structures, enhancing megafaunal abundance, providing source populations for the open slope, and enhancing local and regional species diversity.

Pelagic amphipods from the North Atlantic Ridge in summer 2004

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The distribution of pelagic amphipods along the North Atlantic Ridge in the open waters, from Azores to Iceland, is analyzed. Samples were collected along the MAR during the Leg 1 of the MAR-ECO cruise by the R.V. 'G.O. Sars' with use of the mid-water trawls between 9 June and 1 July 2004. Forty seven species (17 gammarids and 30 hyperiids) were found including *Lanceola laticarpa*, a new record for the Atlantic Ocean. In order to study the structure of the amphipod assemblages on a large geographic scale we used Cluster analysis and the non-metric Multidimensional scaling (MDS). ANOSIM tests revealed that of the five factors investigated the hydrographic region were the most important (global $R = 0.301$, $p < 0.1\%$), followed by ridge section (global $R = 0.293$, $p < 0.1\%$) and depth zone (global $R = 0.195$, $p < 0.1\%$). The strongest difference were found between the northern hydrographical region (Modified North Atlantic Water, MNAW) and the two southern regions: North Atlantic Central Water (NACW, $R = 0.525$, $p < 0.1\%$) and Sub-Polar Front (SPF, $R = 0.408$, $p < 0.1\%$). The null hypotheses (no differences between groups) could not be rejected for position relative to ridge axis, ($p < 48\%$) or solar cycle ($p < 9.7\%$). The spatial distribution of the cluster groups of amphipod species shows a higher spatial variation in the upper 750 m, compared to the deeper layers. The Subpolar front influenced the assemblage structure in the upper layers, separating 4 groups to the North from 2 groups to the South of the frontal region. Below 750 m there was a widespread deep-living species assemblage (one cluster), extending from the Reykjanes Ridge in the north to the Azorean zone in the south.

Cold-water coral distributions in the Drake Passage from towed camera observations – the nbp08-05 expedition

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Seamounts represent unique deep-sea features, creating habitats that have often been described as having high levels of endemism, highly productive fisheries and benthic communities vulnerable to anthropogenic impacts. The difficulties in sampling in the Drake Passage (high winds, intense storms and strong currents) have led to a paucity of information on habitats in this area, particularly those on seamounts and ridges. Previously, no cruises had been specifically directed at imaging or sampling deep-water corals from the Southern Ocean and so it is likely that the species composition, densities, and ranges are vastly underestimated in this region. In May 2008 the RV Nathaniel

B. Palmer 08-05 expedition set out to locate and sample deep-water corals in the Drake Passage. During this expedition a combination of multi-beam swath bathymetry, WHOI TowCam photographs, environmental water chemistry, geographic data, dredges and trawls were used to find, sample and map cold-water coral locations and habitats.

Six main areas were explored during this cruise – Elephant Island (water depths 450 m and 2000 m), Southern Shackleton Fracture Zone (750 m), “Interim” Seamount (1100 m, 1420 m) and Sars Seamount (600m). In total 36 species of coral were collected (Stylasterid, Octocorallia and Scleractinia) and over 8000 digital still images along a total of 16 km of seafloor were taken with the WHOI TowCam system. These images were assessed for biota and bottom type during the cruise allowing characterization of the areas where deep-water corals live in this extreme environment. Each of the six locations sampled in the Drake Passage showed little similarity in faunal diversity with the other five locations, highlighting how little we understand these isolated features and how they might form biological stepping stones between the Polar and South American continental shelves.

Methodological advances in ancient DNA techniques for cold-water corals: utility for phylogenetic studies

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The field of Ancient DNA is relatively young, and it is only in the last five years that its application has been tried and tested on fossil scleractinian coral material. The ability to extract DNA from coral material that predates historical science sailing voyages could revolutionize our understanding of taxonomy, biogeography and evolution of corals and coral

reefs from tens of thousands of years in the past. Deep-sea corals in particular present interesting subjects for ancient DNA techniques. They have been present throughout the world's oceans for millions of years, and so have experienced many climatic changes and extinction events. Their modern distribution is mainly controlled by a combination of these historical changes and by physical (e.g. ocean currents, suitability of substrate) and biological (e.g. recruitment, trophic) factors. Importantly for ancient DNA studies, they have also been preserved in cool dark conditions, often protected from extensive organismal damage by layers of sediment.

In 2007 we published data on the ability to extract DNA from ancient cold-water corals (Waller et al., 2007). Since that time our extraction and purification methods have improved several-fold, allowing DNA to be extracted from more ancient samples and species. This paper presents our methodological advances using adapted demineralization and purification techniques, and presents new phylogenetic data on ancient cold-water corals from the Mediterranean and outer Atlantic. By improving methodology to work with both more samples and less starting material, these techniques could now be applied to rare museum specimens, where type material DNA is not available, and would be highly valuable.

Design of marine protected areas for nodule mining in the abyssal Pacific using principles of ecosystem based management

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Abyssal nodule mining in the Clarion-Clipperton Fracture Zone (CCZ) will affect large areas by direct mining disturbance and redeposition from sediment plumes. Benthic ecosystem recovery is expected to be very slow, requiring decades for the soft-sediment fauna and thousands to millions of years for biota specializing on manganese nodules. Because of the large spatial scales and long duration of potential mining impacts, it is extremely desirable to use spatially based ecosystem management to safeguard seafloor biodiversity in the CCZ. A workshop of 25 experts was tasked with applying principles of ecology and ecosystem management to design a network of marine protected areas (MPAs) for the CCZ. The workshop recommended that one 400 x 400 km MPA be placed in each of nine subregions of the CCZ to meet the following six goals:

- 1) Protect 30-50% of the management area (CCZ).
- 2) Each MPA should capture the full range of habitat variability within a region (nodule fields, sediment plains, seamounts, scarps, etc.).
- 3) Each MPA should capture the minimum viable population sizes for most components of the fauna to "ensure persistence of representative fauna" (yielding a core area 200 km x 200 km).
- 4) MPAs should be replicated across the region to capture N-S and E-W turnovers of biota (forced by gradients in overlying primary productivity).

5) Each MPA should be large enough to buffer the core region from the impacts of mining sediment plumes (buffer zone of 100 km).

6) MPAs should be integrated into the existing ISA framework of mining claims, without compromising scientific principles.

Geomorphologic, oceanographic, current ecological, and human-dimension information were incorporated into a Geographical Information System (GIS) database. GIS analyses then allowed optimization of MPA locations to maximize protection of seamounts within a subregion and to minimize overlap with existing mining claim areas.

Report about two new species of Pruvoinidae (Mollusca, Solenogastes, Cavibelonia) from the DIVA-Artabria I (02-03) Expeditions

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The DIVA-Artabria I (02-03) Expeditions have as their main aim the study of the biodiversity of the bathial deep-sea benthos in the western coast of Galicia (NW Spain) in depths between 100-1000 m. In spite of the high biodiversity of medium to large molluscs in NW Atlantic waters, which have been relatively well surveyed, only a little is known about the small Mollusca of this region, as the Solenogastres. These small marine vermiform molluscs have an aculiferous mantle covered with calcareous sclerites, a ventral pedal groove and a subterminal cavity. They are not a rare animal group since they are present on most marine bottoms, from coastal areas to great depths. The family Pruvotinidae is made up of fifteen genera. In this communication we present the first data about two new species of *Pruvotina* Cockerell, 1903 and *Gephyroherpia* Salvini-Plawen, 1978 collected at a depth of 600-1200 m. *Pruvotina* sp. NW Spain (43°57.03'N; 8°54.795'W). Water depth: 1191-1132 m. Body up to 3.2 mm x 0.5 mm. Thick cuticle (35-50 µm). With hollow hook-shaped sclerites. Mouth opening separated from atrium. Distichous radula with four denticles. With dorso-pharyngeal papilla gland. Ventral foregut glandular organs of type A with short and wide ducts. Without oesophagus. Dorso-anterior caecum impair. With vesicle and receptacle seminal. Unpaired secondary genital opening. Without abdominal spines. Without copulatory stylets 14 gill folds. A dorso-terminal sense organ. *Gephyroherpia* sp. NW Spain (43°48.587'N; 08°51.402'W). Water depth: 598-610 m. Body up to 7 mm x 0.8 mm. With dorsal keels. Thick cuticle (40-50 µm). With hollow hook-shaped sclerites. Mouth opening separated from atrium. Distichous radula without denticles. Without dorso-pharyngeal papilla gland. Ventral foregut glandular organs of type A with long ducts. Oesophagus with glands. Dorso-anterior caecum impair. Unpaired secondary genital opening. With receptacula seminis. Without abdominal spines. Without copulatory stylets. 15 gill folds. A dorso-terminal sense organ.

Spatial and temporal changes in the deep-water community Copepods composition in the Catalan sea.

Zucca L., Cartes J.E. and Jaume D.

Summary

Zooplankton as dominant taxa in copepods occupy a key position in pelagic foodweb, as they transfer organic energy produced by phytoplankton to higher trophic levels, including pelagic fish. Changes in deep-water community composition, in the vertical and horizontal distribution of Copepods were studied in the Catalan sea in 2006-2007 comparing also with samples taken in 1966-1967 in the same area. Samplings were carried out in 4 stations, both at ca.600-800 m depth. Net differed in mesh size in 1966 (150 and 200 μ) and in 2007 (500 μ) both dotted with an opening-closing system. CTD profiles were also performed taking T, S, fluorescence and turbidity as environmental variables in 2007. In this year we took samples also in the water-column sediment interface using a Macer-GIROQ suprabenthic sludge (500 μ). Copepods were counted and classified into 23 mainly families. In 2007 Copepods were different regarding dominant species in the WP2 samples (*Calanus helgolandicus*, *Gaetanus armiger*, *Euchaeta marina*) and in the suprabenthos (*Candacia armata*, *Candacia tenuimana*, *Aetidopsis multiserrata*). Comparing with old data (Vives et al., 1967) dominant species in the water column in 1966-1967 were *Calanus helgolandicus*, *Centropages typicus*, *Temora stylifera*. and *Pleuromamma abdominalis*. Long term differences will be interpreted considering the different mesh size used, also discussing possible influence of environmental factors.

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